

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:41:41 ; Search time 1852.19 Seconds
(without alignments)
909.372 Million cell updates/sec

Title: US-09-801-371A-1
Perfect score: 104
Sequence: 1 gaattcaactggggcctcc.....ggtctgcaggaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	104	100.0	722 14	BQ007008	BQ007008 UI-H-E11-
C 2	104	100.0	1014 9	AL543083	AL543083 AL543083
C 3	103	99.0	248 14	T29839	T29839 EST97164 Hu
C 4	86	82.7	581 9	AI242177	AI242177 qh81908.x
C 5	85	81.7	561 12	BG232086	BG232086 naf32e06
C 6	61.4	59.0	660 9	AL575811	AL575811 AL575811

C 7	61.2	58.8	564 9	AA69697	AA69697 z178f12.s
C 8	60.8	58.5	562 9	AA207062	AA207062 z178f03.s
C 9	48.2	46.3	546 9	AA824594	AA824594 oc83d11.s
C 10	34.8	33.5	136 17	B38591	B38591 HS-1047-B2-
C 11	32.6	31.3	691 9	AL110410	AL110410 DKFZp434K
C 12	32.6	31.3	888 14	BQ232100	BQ232100 AGENCOURT
C 13	32.2	31.0	342 12	BF407522	BF407522 UI-R-BJ2-
C 14	31.8	30.6	876 17	CNS001YT	AL075400 Drosoph11
C 15	30.4	29.2	446 10	BB840094	BB840094 BB840094
C 16	30.4	29.2	452 9	AI286591	AI286591 uk04d09.y
C 17	30.4	29.2	547 9	AA073604	AA073604 mm96902.r
C 18	30.4	29.2	679 14	BQ769691	BQ769691 UI-M-F10-
C 19	30.4	29.2	711 14	BQ179477	BQ179477 UI-M-EW0-
C 20	30.4	29.2	721 17	AZ839536	AZ839536 2M0135P07
C 21	30.4	29.2	792 13	BI454418	BI454418 603170772
C 22	30.4	29.2	1038 14	BQ963825	BQ963825 AGENCOURT
C 23	30.2	29.0	430 9	AA117760	AA117760 mo65c07.r
C 24	29.8	28.7	768 17	BH027439	BH027439 RPCI-24-3
C 25	29.8	28.7	981 13	BM470874	BM470874 AGENCOURT
C 26	29.2	28.1	266 10	BE020334	BE020334 sm40d12.y
C 27	29.2	28.1	383 12	BE807705	BE807705 ss29c03.y
C 28	29.2	28.1	460 10	BE611325	BE611325 sq79d11.y
C 29	29.2	28.1	484 9	AJ003317	AJ003317 AJ003317
C 30	29.2	28.1	491 9	AL587755	AL587755 AL587755
C 31	29.2	28.1	506 10	AW704380	AW704380 sk30d04.y
C 32	29.2	28.1	525 14	BM954069	BM954069 sam69q09.y
C 33	29.2	28.1	885 12	BE873485	BE873485 601450395
C 34	29.2	28.1	1021 17	CNS04LE6	AL296007 Tetradon
C 35	29.2	27.9	509 17	AQ731196	AQ731196 HS_5531_A
C 36	29.2	27.9	589 9	AL682708	AL682708 AL682708
C 37	29.2	27.9	589 9	AL792732	AL792732 AL792732
C 38	29.2	27.9	604 9	AL678840	AL678840 AL678840
C 39	29.2	27.9	616 9	AL655516	AL655516 AL655516
C 40	29.2	27.9	638 9	AL642049	AL642049 AL642049
C 41	29.2	27.9	643 9	AL659308	AL659308 AL659308
C 42	29.2	27.9	658 17	AZ656161	AZ656161 LM0531J03
C 43	29.2	27.9	690 9	AL632106	AL632106 AL632106
C 44	29.2	27.9	701 9	AL636546	AL636546 AL636546
C 45	29.2	27.9	1014 14	BQ942135	BQ942135 AGENCOURT

ALIGNMENTS

RESULT 1
BQ007008/c 722 bp mRNA linear EST 26-MAR-2002
UI-H-E11-azb-j-22-0-UI.s1 NCL_CGAP_E11 Homo sapiens CDNA clone
IMAGE:5846517 3', mRNA sequence.

ACCESSION BQ007008 GI:19731908
VERSION BQ007008.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 722)
JOURNAL NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this CDNA
sequence: 297-371, >(TAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1. 722
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5846517"
/clone_lib="NCI_CGAP_E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
ACACTTGCAC.
TAG_LIB=UI-H-E11
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTGCAC"

BASE COUNT 204 a 162 c 164 g 190 t 2 others
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 595 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 536
OY 61 GAATCTGGAGACGAGGAGCCTTTGTTCTGGCCAGATGCTGC 104
|||||
Db 535 GAATCTGGAGACGAGGAGCCTTTGTTCTGGCCAGATGCTGC 492

RESULT 2
AL543083/c
LOCUS AL543083 1014 bp mRNA linear EST 16-FEB-2001
DEFINITION AL543083 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1002YE03 3
prime, mRNA sequence.
ACCESSION AL543083
VERSION AL543083.1 GI:12875561
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1014)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 1014
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1002YE03"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 265 a 232 c 281 g 234 t 2 others
ORIGIN

Query Match 100.0%; Score 104; DB 9; Length 1014;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 552 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 493
OY 61 GAATCTGGAGACGAGGAGCCTTTGTTCTGGCCAGATGCTGC 104
|||||
Db 492 GAATCTGGAGACGAGGAGCCTTTGTTCTGGCCAGATGCTGC 449

RESULT 3
T29839
LOCUS T29839 248 bp mRNA linear EST 06-SEP-1995
DEFINITION EST97164 Human Testis Homo sapiens cDNA 5' end similar to tumor necrosis factor, alpha (HT:1190), mRNA sequence.
ACCESSION T29839
VERSION T29839.1 GI:611937
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 248)
AUTHORS Adams, M.D., Kerlavage, A.R., Fieischmann, R.D., Fulmer, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Kelley, J.M., Kimek, R.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
JOURNAL Based Upon 83 Million Basepairs of cDNA Sequence
MEDLINE Nature 377, 3-174 (1995)
COMMENT 96026280
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
Location/Qualifiers
1. 248
/organism="Homo sapiens"
/db_xref="ATCC (inhost):107667"
/db_xref="taxon:9606"
/clone_lib="Human Testis"
/note="Organ: testis"

	BASE COUNT	63 a	65 c	60 g	57 t	3 others
	ORIGIN					
	Query Match	99.0%; Score 103; DB 14; Length 248;				
	Best Local Similarity	99.0%; Pred. No. 3e-22;				
	Matches	103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
OY	1 GAATTCAAACTGGGCGCTCCAGAACCTCACTGGGGGCCCTACAGCTTTGATCCCTGCATCATGTG 60					
Dd	58 GAATTCAAACTGGGCGCTCCAGAACCTCACTGGGGGCCCTACAGCTTTGATCCCTGCATCATGTG 117					
OY	61 GAATCTGAGACCAGGAGCCTTGTCTTGCTGGCCAGAATGCTGC 104					
Dd	118 GAATCTNGAGACCAGGAGCCTTGTCTTGCTGGCCAGAATGCTGC 161					
RESULT 4						
A1242177/c	A1242177 581 bp mRNA linear EST 01-DEC-1998					
LOCUS	qH8I908.xl Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens CDNA					
DEFINITION	clone IMAGE:1851134 3' similar to gb:M10988 TUMOR NECROSIS FACTOR PRECURSOR (HUMAN);, mRNA sequence.					
ACCESSION	A1242177					
VERSION	A1242177.1 GI:3837574					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 581)					
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.					
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
JOURNAL	Unpublished (1997)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert length: 1280 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 463. Location/Qualifiers 1. .581 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1851134" /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dt) primer [5' AACTGAAGAATAATTAAAGATCTTTTTTTTTTTTTTTT 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."					
FEATURES						
source						
BASE COUNT	179 a	130 c	135 g	137 t		
ORIGIN						
Query Match	82.7%; Score 86; DB 9; Length 581;					
Best Local Similarity	90.2%; Pred. No. 9.3e-17;					
Matches	92; Conservative 0; Mismatches 10; Indels 0; Gaps 0;					
OY	3 ATTCAAACTGGGCGCTCCAGAACCTCACTGGGGGCCCTACAGCTTTGATCCCTGCATCATGTGA 62					
	I I I I					
Dd	579 AATTCAAACTGGGCGCTCCAGAACCTCACTGGGGGCCCTACAGCTTTGATCCCTGCATCATGTGA 520					
OY	63 ATCTGAGACCAGGAGCCTTGTCTTGCTGGCCAGAAATGCTGC 104					

[illegible]

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 660)
TITLE Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 660
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1070Y015"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 251 a 90 c 103 g 158 t 58 others
ORIGIN

Query Match 59.0%; Score 61.4; DB 9; Length 660;
Best Local Similarity 68.9%; Pred. No. 5.5e-09;
Matches 71; Conservative 8; Mismatches 24; Indels 0; Gaps 0;

OY 2 AATTCAACTGGGGCTCCAGACTGAGCTGGGCTTGTGATCCCTGACATCTGG 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 526 AATTCAACTGTTCTCCATCTACATCTTCTTCTTATCCCTTACATCTTT 467

OY 62 AATCTGAGACGAGGAGGAGGCTTTGGTCTGCGCAGATGCTGC 104
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 466 AATCTTATACCATTTATSTTTTSTTTSTGSSAGATGCTGS 424

RESULT 7
AA699697/c 564 bp mRNA linear EST 19-DEC-1997
LOCUS z178f12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
DEFINITION clone IMAGE:446927 3' similar to gb:M10988 TUMOR NECROSIS FACTOR
PRECURSOR (HUMAN);, mRNA sequence.
AA699697
AA699697.1 GI:2703844
EST.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 564)
TITLE Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
JOURNAL WashU-NCI human EST Project
COMMENT Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 397.

FEATURES
source
1. 564
/organism="Homo sapiens"
/db_xref="GDB:1351184"
/db_xref="taxon:9606"
/clone="IMAGE:446927"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGAGAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 176 a 123 c 138 g 127 t
ORIGIN

Query Match 58.8%; Score 61.2; DB 9; Length 564;
Best Local Similarity 85.1%; Pred. No. 6e-09;
Matches 80; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

OY 2 AATTCAACTGGGGCTCCAGACTGAGCTGGGCTTGTGATCCCTGACA-TCG 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 564 AATTCAACTGGGGCTCCAGACTGAGCTGGGCTTGTGATCCCTGACA-TCG 505

OY 61 GAATCTGAGACGAGGAGGAGGCTTTGGTCTGCGC 94
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 504 ACATCTGAGACGAGGAGGAGGCTTTGGTCTGCGC 471

RESULT 8
AA207062/c 562 bp mRNA linear EST 13-AUG-1997
LOCUS z178b03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682637 3'
DEFINITION similar to gb:M10988 TUMOR NECROSIS FACTOR PRECURSOR (HUMAN);, mRNA
sequence.
AA207062
AA207062.1 GI:1802411
EST.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 562)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 412.

FEATURES
source
1. 562
/organism="Homo sapiens"
/db_xref="GDB:5585957"
/db_xref="taxon:9606"
/clone="IMAGE:682637"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"

BASE COUNT	155 a	138 c	110 g	143 t	16 others
ORIGIN	/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCATTTTCTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."				
Query Match	58.5%;	Score 60.8;	DB 9;	Length 562;	
Best Local Similarity	87.8%;	Pred. No. 7.9e-09;			
Matches	65;	Conservative	0;	Mismatches	9;
				Indels	0;
				Gaps	0;
QY	31	GGGGCTACAGCTTTGATCCTGACATCTGGAATCTGAGACACGAGGACCTTTGGTCT	90		
Db	558	GGGCTACCGCTTGNATCCCTGACATCTGAAATCTGAGACACGAGGACCTTTGGTCT	499		
QY	91	GGCCAGAAATGCTGC	104		
Db	498	GGCCAGAAATGCTGC	485		
RESULT 9					
AA824594/c	546 bp mRNA linear EST 18-MAR-1998				
LOCUS	oc83d11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1356309				
DEFINITION	similar to gb:MI0988 TUMOR NECROSIS FACTOR PRECURSOR (HUMAN);, mRNA sequence.				
ACCESSION	AA824594				
VERSION	AA824594.1 GI:2896616				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 546)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 614 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 443. Location/Qualifiers 1. 546 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1356309" /clone_lib="NCI_CGAP_GCB1" /tissue_type="germinal center B cell" /lab_host="DH10B" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-),				
FEATURES					
source					

Query Match	Best Local Similarity	Score	DB	Length
Matches	53; Conservative	46.3%; 86.9%;	0; Mismatches	8; Indels
			0; Gaps	0;
Db	44	TTGATCCCTGACATCTGGAATCTGGAGACCGAGGAGCCCTTTGGTCTCTGGCCAGAATCTG	103	
	546	TTGATCCCGAACATCTGGAATCCGGAGACCCACGAGCCCTTGGTCTGCCCAGATTGCTG	487	
OY	104	C	104	
Db	486	C	486	
RESULT 10				
B38591				
LOCUS	B38591	136 bp	DNA	linear
DEFINITION	HS-1047-B2-G12-MF.ab1 CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=24 Row=N, DNA sequence.			
ACCESSION	B38591			
VERSION	B38591.1	GI:2542843		
KEYWORDS	GSS.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 136)			
AUTHORS	Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.			
TITLE	Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors			
JOURNAL	Unpublished (1997)			
COMMENT	Contact: Mahairas GG, Zackrone KD, Hood L University of Washington Seattle, WA 98195, USA Tel: (206) 616-8744 Fax: (206) 685-7301 Email: kzackrone@u.washington.edu Sequence Tagged Connector Plate: CT 830 row: N column: 24 Class: BAC ends High quality sequence stop: 136.			
FEATURES				
source	1. .136 Location/Qualifiers /organism="Homo sapiens" /db_xref="taxon:9606" /clone="Plate=CT 830 Col=24 Row=N" /clone_lib="CIT Human Genomic Sperm Library C" /sex="M" /note="Organ: sperm; Vector: pBelOBAC11; BAC clones in E-Coli DH10B"			
BASE COUNT	32 a	33 c	35 g	34 t
ORIGIN				2 others
Query Match	33.5%;	Score 34.8;	DB 17;	Length 136;
Best Local Similarity	62.1%;	Pred. No. 0.73;		
Matches	54; Conservative	0; Mismatches	33; Indels	0; Gaps
OY	8	AACTGGGCGCTCAGAACTCACTGCGGCGCTTACAGCTTTGATCCCTGACATCTGGAATCTG	67	
	14	ACCGNGATCTCTAGAGTGCAGTCGACGATGCAGCTTCAACTGTGTGCTGCGGCAATGTG	73	

tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized heart library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-41, >AT_rich#Low_complexity 165-257, >B1_MM#SINE/Alu
Seq primer: M13 Forward
POLYA=yes.

FEATURES
source Location/Qualifiers
1..342

/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ2-bqt-c-05-0-UI"
/clone_1lb="UI-R-BJ2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pUT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2 library is a subtracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15 dpc, AV canal at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=UI-R-BJ2
TAG_TISSUE=heart
TAG_SEQ=ACCAAC"

BASE COUNT 83 a 73 c 66 g 120 t
ORIGIN

Query Match 31.0%; Score 32.2; DB 12; Length 342;
Best Local Similarity 63.6%; Pred. No. 6.8;
Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 21 AGAAGTCACTGGGGCTACAGCTTGATCCCTGACATCTGGAATCTGAGACCAAGCAGC 80

Db 277 AGACAGAGCTGGGGCTAGACCTGTATCTCCAGTATCTGGAGGTGAGGCGAGCGCAT 218

QY 81 CTTTGTTCTGCCAGA 97

Db 217 CTAAGTTTGAGGCCAGA 201

RESULT 14
CNS001YJ

LOCUS 876 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR37K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL075400
VERSION AL075400.1 GI:4955180

KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 876)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's Laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source Location/Qualifiers
1..876

/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR37K10"
/clone_1lb="RPCI-98"
/note="end : T7"

BASE COUNT 162 a 239 c 233 g 214 t 28 others
ORIGIN

Query Match 30.6%; Score 31.8; DB 17; Length 876;
Best Local Similarity 50.5%; Pred. No. 13;
Matches 51; Conservative 10; Mismatches 40; Indels 0; Gaps 0;

QY 3 ATTCAACTGGGGCTCCAGACTCACTGGGGCTTGCATCCCTGACATCTGA 62

Db 29 ATTCTMAHBGTCGTGCGCTCTTGMGGGATMTTAAADTTMTCAATACATCGAG 88

QY 63 ATCTGAGACCAAGGAGCCCTTTGTTCTTGCCAGATGCTG 103

Db 89 AGGTGGCGTCCACTGTACCAKTTGGTCAGGCGCGTCTCTG 129

RESULT 15
BB840094

LOCUS 446 bp mRNA linear EST 21-NOV-2001
DEFINITION BB840094 RIKEN full-length enriched, 12 days embryo whole body Mus musculus cDNA clone E970004M24 5', mRNA sequence.

ACCESSION BB840094
VERSION BB840094.1 GI:17040825
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 446)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akaira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagl,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 18:32:14 ; Search time 239.837 Seconds
(without alignments)
976.530 Million cell updates/sec

Title: US-09-801-371A-1
Perfect score: 104
Sequence: 1 gaattcaactggtggcctcc.....ggttcgtgccagatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*

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2:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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10:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
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23:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	104	100.0	104	21	AAZ99816	Cis-acting nucleot
2	104	100.0	787	20	AAZ20979	Human TNFalpha 3'U
3	104	100.0	1275	7	AAAG60558	Sequence encoding
4	104	100.0	1323	7	AAAG60363	Sequence encoding
5	104	100.0	1324	21	AAAF21085	Human low adenosin
6	104	100.0	1324	21	AAA34963	Human adenosine re
7	104	100.0	1560	9	AAAG0219	Sequence of pE4 en
8	104	100.0	1585	7	AAAG60557	Sequence encoding
9	104	100.0	1606	7	AAAG60446	Sequence encoding

10	104	100.0	1606	17	AAAT15424	Human tumour necro
11	104	100.0	1643	17	AAAT31021	Human tumour necro
12	104	100.0	1643	24	ABRI3195	Human tumour necro
13	104	100.0	2270	20	AAZ20983	Chimeric nucleic a
14	104	100.0	2570	20	AAZ20984	Chimeric nucleic a
15	104	100.0	3634	19	AAV39005	TNF-alpha gene use
16	104	100.0	3634	20	AAV39005	Tumour necrosis fa
17	104	100.0	3634	21	AAAC63770	Human TNF-alpha ge
18	104	100.0	3634	21	AAAA40760	Human tumour necro
19	104	100.0	7112	22	AAAF86085	Lymphotoxin and tu
20	104	100.0	7112	22	AAAF57450	Human tumour necro
21	104	100.0	16310	21	AAAF21086	Human low adenosin
22	104	100.0	16310	21	AAA34964	Human adenosine re
23	104	100.0	17634	21	AAAF21087	Human low adenosin
24	104	100.0	17634	21	AAAF21087	Human adenosine re
25	104	100.0	17634	21	AAA34965	Human adenosine re
26	104	100.0	17634	21	AAA34965	Human adenosine re
27	104	100.0	81800	24	ABK84756	Human CDNA differe
28	102.4	98.5	817	11	AAQ04340	THP-1, Homo sapie
29	102.4	98.5	818	10	AAAN91035	XhoI - petI sectio
30	102.4	98.5	1200	8	AAAT0072	Human anti-tumor p
31	102.4	98.5	1200	10	AAAN90969	Part of gene for a
32	102.4	98.5	1585	7	AAAG60527	Sequence encoding
33	102.4	98.5	1585	15	AAQ58037	Tumor necrosis fac
34	102.4	98.5	1643	8	AAAT1307	Sequence encoding
35	91.8	88.3	815	8	AAAT70075	Human anti-tumor p
36	50	48.1	50	21	AAZ99815	Sequence of the st
37	43	41.3	43	21	AAZ99817	Cis-acting nucleot
38	33	31.7	51	21	AAZ99916	Sequence of the st
39	31.4	30.2	10240	19	AAV39007	Porcine TNF-alpha
40	30.2	29.0	2980	22	AAK86235	Human immune/haema
41	29.2	28.1	37664	22	AAK83781	Human immune/haema
42	29.2	28.1	61710	22	AAK83782	Human immune/haema
43	28.4	27.3	15650	22	ABA15903	Human nervous syst
44	28.4	27.3	15650	22	ABA16364	Human nervous syst
45	28.2	27.1	585	22	AAH11269	Human CDNA clone (

ALIGNMENTS

RESULT 1	
AAZ99816	
ID	AAZ99816 standard; RNA; 104 BP.
XX	AAZ99816;
AC	
XX	
DT	12-JUL-2000 (first entry)
XX	
DE	Cis-acting nucleotide sequence derived from human TNF-alpha.
XX	
KW	Cis-acting sequence; Intron removal; trans-acting factor; alpha-subunit;
KW	RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW	tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200014255-A1.
XX	
PD	16-MAR-2000.
XX	
PF	06-SEP-1999; 99WO-IL00483.
XX	
PR	07-SEP-1998; 98IL-0126112.
PR	26-OCT-1998; 98IL-0126757.
XX	
PA	(YISS) YISSUM RES & DEV CO.
XX	
PI	Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX	
DR	WPI; 2000-257000/22.
XX	
PT	Regulation of gene expression by mRNA splicing is carried out using a

PT cis-acting nucleotide sequence controlled by phosphorylation of the
PT alpha-subunit of eukaryotic initiation factor 2 -
XX
PS Claim 4; Page 15; 75pp; English.
XX
CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a
CC gene which harbours at least one cis-acting nucleotide sequence. This
CC removal is effected during the production of mRNA of the gene, and
CC depends on activation of a trans-acting factor which is an RNA-activated
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2. (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can
CC be used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a cis-acting nucleotide sequence of the
CC invention.
XX
SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 other;
Query Match 100.0%; Score 104; DB 21; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTGTGATCCCTGACATCTG 60
Db 1 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTGTGATCCCTGACATCTG 60
QY 61 GAATCTGGAGACGAGGAGCCCTTGTGTTCTGCGCCAGAAATGCTGC 104
Db 61 GAATCTGGAGACGAGGAGCCCTTGTGTTCTGCGCCAGAAATGCTGC 104
RESULT 2
AAZ20979
ID AAZ20979 standard; DNA; 787 BP.
XX
AC AAZ20979;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human TNFalpha 3'UTR.
XX
KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW psoriasis; graft versus host disease; lupus erythematosus;
KW diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
XX
OS Homo sapiens.
XX
PN WO9943840-A1.
XX
PD 02-SEP-1999.
XX
PF 12-JAN-1999; 99WO-US00637.
XX
PR 27-FEB-1998; 98US-0076316.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Tatake RJ, Marlin SD, Barton RW;
XX
DR WPI; 1999-527630/44.
XX
PT A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
PT promoter and an apoptosis-inducing Granzyme B polynucleotide -
XX
PS Example 1; Page 60-61; 71pp; English.

XX
CC This sequence represents a human TNFalpha (tumour necrosis factor alpha)
CC 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984)
CC were constructed comprising at least one TNFalpha promoter enhancer
CC region (AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA
CC encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a
CC TNFalpha 3'UTR sequence. TNFalpha is one of a number of
CC cytokines produced by inflammatory cells. Upregulation and/or
CC dysregulation of cytokines in inflamed tissue may be directly or
CC indirectly responsible for exacerbation of chronic inflammatory
CC diseases. Introduction of the chimeric nucleotide to activated
CC inflammatory cells causes them to undergo apoptosis. Pharmaceutical
CC compositions of the chimeric nucleotide may be useful for treating
CC inflammatory disorders such as multiple sclerosis, Crohn's disease,
CC ulcerative colitis, psoriasis, graft versus host disease, lupus
CC erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing
CC spondylitis, and in particular, rheumatoid arthritis. The use of such
CC chimeric nucleotides offers simpler and cheaper long-term relief, in
CC comparison with existing conventional pharmaceutical and invasive surgery
CC methods.
XX
SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 other;
Query Match 100.0%; Score 104; DB 20; Length 787;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTGTGATCCCTGACATCTG 60
Db 222 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTGTGATCCCTGACATCTG 281
QY 61 GAATCTGGAGACGAGGAGCCCTTGTGTTCTGCGCCAGAAATGCTGC 104
Db 282 GAATCTGGAGACGAGGAGCCCTTGTGTTCTGCGCCAGAAATGCTGC 325
RESULT 3
AAN60558
ID AAN60558 standard; DNA; 1275 BP.
XX
AC AAN60558;
XX
DT 28-JUL-1991 (first entry)
XX
DE Sequence encoding mature human tumour necrosis factor (hTNF) mutein
DE Ser 69 in PAW731.
XX
KW Antitumour; anticancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..474
FT /*tag- a
XX
PN WO8604606-A.
XX
PD 14-AUG-1986.
XX
PF 03-FEB-1986; 86WO-US00236.
XX
PR 07-FEB-1985; 85US-0698939.
PR 19-OCT-1982; 82US-0435154.
PR 15-APR-1983; 83US-0486162.
PR 20-DEC-1983; 83US-0564224.
PR 15-OCT-1984; 84US-0661026.
PR 07-FEB-1985; 85US-0695934.
XX
PA (CETU) CETUS CORP.
XX
PI Mark DF, Lin LS, Lu SDY, Wang AM;
XX
DR WPI; 1986-225458/34.

DR P-PSDB; AAP60656.
XX
PT New synthetic muteins of human tumour necrosis factor protein
PT are obtd. by direct mutagenesis and retain antitumour activity
XX
PS Disclosure; Fig 3a; 47pp; English.
XX
CC The sequence encoding TNF produced by the promyelocytic leukemia
CC cell line (HL-60, ATCC no. CCL240) has been cloned and expressed in
CC E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
CC the TNF sequence appears to be involved in disulphide linkages. The
CC patentors claim a novel synthetic mutein of a biologically active
CC hTNF protein, having at least one cysteine residue free from a
CC disulphide link and non-essential to the activity and having at
CC least one of the cysteine residues deleted or replaced by another AA.
XX Plasmid pAW731 (Ser 69) is claimed.
XX
SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 other;
SQ
Query Match 100.0%; Score 104; DB 7; Length 1275;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 60
Db 693 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 752
QY 61 GAATCTGGAGACGAGGAGAGCCCTTGGTCTGCGCCAGAAATGCTGC 104
Db 753 GAATCTGGAGACGAGGAGAGCCCTTGGTCTGCGCCAGAAATGCTGC 796

RESULT 4
AAN60363
ID AAN60363 standard; DNA; 1323 BP.
XX
AC AAN60363;
XX
DT 19-JUN-1991 (first entry)
XX
DE Sequence encoding human tumour necrosis factor.
XX
KW hTNF; tumour; cancer; interferon; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..534
FT sig_peptide /tag= a
FT /tag= b
FT mat_peptide /label= Secretory leader peptide
FT 61..534
FT /tag= c
XX
PN EPI68214-A.
XX
PD 15-JAN-1986.
XX
PE 03-JUL-1985; 85EP-0304758.
XX
PR 03-DEC-1984; 84US-0677454.
PR 05-JUL-1984; 84US-0627959.
PR 05-JUL-1984; 84US-0628059.
PR 05-JUL-1984; 84US-0628060.
PR 03-DEC-1984; 84US-0677156.
PR 03-DEC-1984; 84US-0677257.
PR 25-JUL-1984; 84US-0627969.
PR 03-DEC-1984; 84US-0677267.
XX
PA (GETH) GENENTECH INC.
XX
PI Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;

XX
DR WPI; 1986-015483/03.
DR P-PSDB; AAP60417.
XX
PT Pure tumour necrosis factor and mutant forms - new DNA coding
PT sequences and transformed cells.
XX
PS Claim 20; Fig 10; 90pp; English.
XX
CC Sequence encodes the pure human tumour necrosis factor, mutants of
CC which are covered by the claims. TNF and mutants are useful in
CC treating tumours, especially in tandem with interferon. The
CC encoding sequence may be used to create plasmid pTRXPATNF, allowing
CC transformation of an E.coli host for the expression of TNF.
XX
SQ Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 other;
SQ
Query Match 100.0%; Score 104; DB 7; Length 1323;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 60
Db 750 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 809
QY 61 GAATCTGGAGACGAGGAGAGCCCTTGGTCTGCGCCAGAAATGCTGC 104
Db 810 GAATCTGGAGACGAGGAGAGCCCTTGGTCTGCGCCAGAAATGCTGC 853

RESULT 5
AAF21085
ID AAF21085 standard; DNA; 1324 BP.
XX
AC AAF21085;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2652.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PE 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 887; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (1) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (1) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;
Query Match 100.0%; Score 104; DB 21; Length 1324;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTGTGATCCCTGACATCTG 60
DB 751 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTGTGATCCCTGACATCTG 810
QY 61 GAATCTGAGACGAGGAGCCTTGTGCTGCGCCAGATGCTGC 104
DB 811 GAATCTGAGACGAGGAGCCTTGTGCTGCGCCAGATGCTGC 854
RESULT 6
AAA34963 standard; DNA; 1324 BP.
XX
AC AAA34963;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2652.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX

PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 814-815; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;
Query Match 100.0%; Score 104; DB 21; Length 1324;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTGTGATCCCTGACATCTG 60
DB 751 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTGTGATCCCTGACATCTG 810
QY 61 GAATCTGAGACGAGGAGCCTTGTGCTGCGCCAGATGCTGC 104
DB 811 GAATCTGAGACGAGGAGCCTTGTGCTGCGCCAGATGCTGC 854
RESULT 7
AAN80219 standard; DNA; 1560 BP.
XX
ID AAN80219
XX
AC AAN80219;
XX
DT 28-DEC-1990 (first entry)
XX
DE Sequence of pE4 encoding human tumour necrosis factor (TNF).
XX
KW Lymphokine; antitumour; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 86..313
FT Location/Qualifiers
FT /*tag= a

FT mat_peptide 314..787
FT /*tag= b
XX W08060625-A.
XX 07-SEP-1988.
PD
XX
XX 25-JAN-1988; 88WO-US00183.
PF
XX
XX 26-FEB-1987; 87US-0019221.
PR
XX
XX (CETU) CETUS CORP.
PA
XX
XX Mark DF, Thomson JW, Lin LS, Yamamoto R;
PI
XX
XX WPI: 1988-271165/38.
DR
XX P-PSDB; AAP80728.
DR
XX
XX Human tumour necrosis factor muteins -
PT having comparable biological activity with improved stability
PT and ease of purification
XX
XX
XX Disclosure; Fig 1-1 to 1-2; 51pp; English.
PS
XX
XX A human TNF protein which is modified from the sequence shown in
CC AAP80728, including naturally occurring allelic variants is claimed. Also
CC claimed are: recombinant DNA sequences encoding the protein (AAN80219)
CC and control sequences for expression; a vector; a transformed host cell;
CC a method of producing the protein by culturing the host cell;
CC pharmaceutical compsn. of the protein and a carrier and a method of
CC treating tumour burden with the compsn. The muteins are capable of the
CC range of biological activities exhibited by native TNF but exhibit
CC improved stability and ease of purification.
XX
XX
SQ Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 other;

Query Match 100.0%; Score 104; DB 9; Length 1560;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGATCCCTGACATCTG 60
DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACACGAGGAGCCTTGTGCTCTGGCCAGAATGCTGC 104
DB 1063 GAATCTGAGACACGAGGAGCCTTGTGCTCTGGCCAGAATGCTGC 1106

RESULT 8
AAN60557
ID AAN60557 standard; DNA; 1585 BP.
XX
XX AAN60557;
AC
XX
XX 28-JUL-1991 (first entry)
DT
XX
XX Sequence encoding mature human tumour necrosis factor (hTNF) in pE4.
DE
XX
XX Antitumour; anticancer; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 86..313
FT /*tag= a
FT mat_peptide 314..787
FT /*tag= b
XX
XX W08604606-A.
PN
XX
XX 14-AUG-1986.
PD
XX

PF 03-FEB-1986; 86WO-US00236.
XX
XX
XX 07-FEB-1985; 85US-0698939.
PR
XX 19-OCT-1982; 82US-0435154.
PR
XX 15-APR-1983; 83US-0486162.
PR
XX 20-DEC-1983; 83US-0564224.
PR
XX 15-OCT-1984; 84US-0661026.
PR
XX 07-FEB-1985; 85US-0695934.
XX
XX
XX (CETU) CETUS CORP.
PA
XX
XX
XX Mark DF, Lin LS, Lu SDY, Wang AM;
PI
XX
XX WPI: 1986-225458/34.
DR
XX P-PSDB; AAP60655.
DR
XX
XX New synthetic muteins of human tumour necrosis factor protein -
PT are obtd. by direct mutagenesis and retain antitumour activity
PT
XX
XX
XX Disclosure; Fig 1; 47pp; English.
PS
XX
XX The sequence encoding TNF produced by the promyelocytic leukemia
CC cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in
CC E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
CC the TNF sequence appears to be involved in disulphide linkages. The
CC patentors claim a novel synthetic mutein of a biologically active
CC hTNF protein, having at least one cysteine residue free from a
CC disulphide link and non-essential to the activity and having at
CC least one of the cysteine residues deleted or replaced by another AA.
CC Plasmid pAW731 (Ser 69) is claimed.
XX
XX
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 other;

Query Match 100.0%; Score 104; DB 7; Length 1585;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGATCCCTGACATCTG 60
DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACACGAGGAGCCTTGTGCTCTGGCCAGAATGCTGC 104
DB 1063 GAATCTGAGACACGAGGAGCCTTGTGCTCTGGCCAGAATGCTGC 1106

RESULT 9
AAN60446
ID AAN60446 standard; cDNA; 1606 BP.
XX
XX AAN60446;
AC
XX
XX 07-AUG-1991 (first entry)
DT
XX
XX Sequence encoding tumour necrosis factor (TNF).
DE
XX
XX Anticancer agent; antitumour; antimalarial; tumour necrosis factor;
KW ss.
XX
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 158..859
FT /*tag= a
FT
XX
XX W08603751-A.
PN
XX
XX 03-JUL-1986.
PD
XX
XX 19-DEC-1985; 85WO-EP00721.
PF
XX
XX 09-OCT-1985; 85US-0785847.
PR
XX 21-DEC-1984; 84US-0684595.
PR

```
PR 09-OCT-1986; 86WO-US02133.
XX
PA (BIOJ ) BIOGEN NV.
PA (FIER/) FIERIS W C.
PA (ALLE/) ALLET B.
PA (BIOG-) BIOGEN INC.
XX
PI Fliers WC, Fransen LM, Tavernier JHL, Marmenout ALM;
PI VanderHeyden J, Allet B, Washima EH;
XX
DR WPI: 1986-182891/28.
DR P-PSDB; AAP60531.
XX
PT Mammalian tumour necrosis factors - produced by culturing
PT pro-karyotic hosts transformed with recombinant DNA
XX
PS Example; Fig 9; 93pp; English.
XX
CC TNF-like polypeptides and compns. are produced by the fermentation
CC of host cells transformed with at least one DNA sequence which codes
CC for a mammalian TNF-like polypeptide operatively linked to an
CC expression control sequence in the transformed host.
XX
SQ Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 other;

Query Match 100.0%; Score 104; DB 7; Length 1606;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTGATCCCTGACATCTG 60
Db 1075 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTGATCCCTGACATCTG 1134

QY 61 GAATCTGGAGACCAAGGAGCCCTTGTGTTCTGGCCAGATGCTGC 104
Db 1135 GAATCTGGAGACCAAGGAGCCCTTGTGTTCTGGCCAGATGCTGC 1178

RESULT 10
AAT15424
ID AAT15424 standard; cDNA; 1606 BP.
XX
AC AAT15424;
XX
DT 23-APR-1996 (first entry)
XX
DE Human tumour necrosis factor cDNA clone p-hTNF-1.
XX
KW Tumour necrosis factor; TNF; phage T4; phage lambda; pL promoter;
KW antitumour; anticancer; antimalarial; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 158..859
FT sig_peptide /tag= a
FT mat_peptide /tag= b
FT 386..856
FT /*tag= c
XX
PN US5487984-A.
XX
PD 30-JAN-1996.
XX
PF 21-DEC-1984; 84US-0684595.
XX
PR 20-DEC-1985; 85US-0811654.
PR 21-DEC-1984; 84US-0684595.
PR 09-OCT-1985; 85US-0785847.
XX
PA (BIOJ ) BIOGEN INC.
XX
```

```
PI Allet B, Kawashima EH;
XX
DR WPI: 1996-105230/11.
DR P-PSDB; AAR88590.
XX
PT Prodn. of tumour necrosis factor - using recombinant DNA encoding
PT TNF under the control of T4 or lambda pL-T4 expression control
PT sequences.
XX
PS Example 9; Fig 9; 43pp; English.
XX
CC A cDNA clone (AAT15424), p-hTNF-1 (DSM 3160), codes for the human
CC tumour necrosis factor (hTNF) precursor (AAR88590). It was obtd.
CC by screening a human cDNA library with a fragment of mouse TNF
CC cDNA. The isolated cDNA may be linked to expression control
CC sequences from phage T4 or phage lambda (see AAT15402-05 and
CC AAT15425-26) for expression in host cells, esp. Escherichia coli,
CC and commercial-scale prodn. of recombinant TNF of use as an
CC antitumour, anticancer and antimalarial agent.
XX
SQ Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 other;

Query Match 100.0%; Score 104; DB 17; Length 1606;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTGATCCCTGACATCTG 60
Db 1075 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTGATCCCTGACATCTG 1134

QY 61 GAATCTGGAGACCAAGGAGCCCTTGTGTTCTGGCCAGATGCTGC 104
Db 1135 GAATCTGGAGACCAAGGAGCCCTTGTGTTCTGGCCAGATGCTGC 1178

RESULT 11
AAT31021
ID AAT31021 standard; DNA; 1643 BP.
XX
AC AAT31021;
XX
DT 26-SEP-1996 (first entry)
XX
DE Human tumour necrosis factor cDNA clone HSTNFR.
XX
KW Gene therapy; hypoxia related enhancer element; HREE; Ischaemia;
KW reperfusion; promoter; tumour necrosis factor; TNF; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 153..854
FT sig_peptide /tag= a
FT 153..854
XX
PN WO9620276-A1.
XX
PD 04-JUL-1996.
XX
PF 13-NOV-1995; 95WO-IB00996.
XX
PR 23-DEC-1994; 94US-0365486.
XX
PA (STRI ) SRI INT.
XX
PI Bishopric NH, Green CJ, Laderoute KR, Murphy B;
PI Webster KA;
XX
DR WPI: 1996-321849/32.
DR P-PSDB; AAW00454.
XX
PT Chimeric gene contg. therapeutic gene linked to HREE - partic. for
PT expressing SOD etc. in hypoxic tissue to reduce tissue injury caused
PT by Ischaemia or reperfusion
```

```
XX PS Example 8; Page 100-101; 118bp; English.
XX CC A PCR-generated DNA fragment (AA731021) encoding human tumour
CC CC necrosis factor (htNF) (AAW00454). htNF induces apoptosis and
CC CC is not known to be induced by hypoxic stress. A -90 bp human
CC CC metallothionein IIA promoter fragment (see also AA731003) was
CC CC inserted upstream of the htNF gene and the construct was used
CC CC to transfect mouse C2C12 myoblasts and A431 cells. Hypoxia-
CC CC mediated TNF induction and tumour control were demonstrated
CC CC in an animal xenograft model.
XX SQ Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;

Query Match          100.0%; Score 104; DB 17; Length 1643;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCCCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 1129
QY 61 GAATCTGAGAGACGAGGAGCCCTTGTGCTTGTGGCCAGAAATGCTGC 104
Db 1130 GAATCTGAGAGACGAGGAGCCCTTGTGCTTGTGGCCAGAAATGCTGC 1173

RESULT 12
ABK13195 standard; DNA; 1643 BP.
XX AC ABK13195;
XX DT 23-APR-2002 (first entry)
XX DE Human tumour necrosis factor alpha (TNF alpha) DNA.
XX KW TNF; apoptosis; ds; tumour; death domain receptor ligand;
KW KW diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1;
KW KW carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma;
KW KW neurological malignancy; haematological malignancy; lichen planus;
KW KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
KW KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
KW KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
KW KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
KW KW discoid lupus erythematosus; human; gene; tumour necrosis factor.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 153..854
FT FT /*tag= a
FT FT /product= "TNF alpha protein"
XX PN US6329148-B1.
XX PD 11-DEC-2001.
XX PF 15-FEB-2000; 2000US-0505250.
XX PR 16-FEB-1999; 99US-120313P.
XX PR 20-AUG-1999; 99US-149989P.
XX PA (STRD ) UNIV LELAND STANFORD.
XX PI Rosen GD, Kao P;
XX XX WPI; 2002-121125/16.
DR P-PSDB; AAU75065.
XX XX Use of a synergistic combination of death domain receptor ligands and
PT diterpenoid triepoxides for killing of tumour cells -
XX XX
```

```
PS Disclosure; Column 27-30; 20pp; English.
XX CC This invention relates to a novel method for enhanced killing of tumour
CC CC cells comprising contacting a tumour cell with a synergistic
CC CC combination of a death domain receptor ligand and a diterpenoid
CC CC triepoxide. This method has cytostatic activity and works by blocking
CC CC TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the
CC CC invention may be used for treating tumours, particularly solid tumours,
CC CC e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma
CC CC also neurological malignancies, haematological malignancies, e.g.
CC CC non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant
CC CC cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma,
CC CC lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia,
CC CC bullous pemphigoid, discoid lupus erythematosus, lichen planus. The
CC CC combination may be administered with other active agents, e.g. anti-
CC CC metastatic, anti-tumour or anti-angiogenic agents. The potent synergy
CC CC between the diterpenoids and the death domain ligands allows increased
CC CC killing at equivalent or lower doses, and can sensitize otherwise
CC CC resistant cells. This sequence represents the human tumour necrosis
CC CC factor alpha (TNF alpha) DNA. TNF alpha is a ligand for death
CC CC domain receptors used in the used method of the invention in
CC CC combination with diterpenoid triepoxides to kill tumours by
CC CC induction of apoptosis.
XX SQ Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;

Query Match          100.0%; Score 104; DB 24; Length 1643;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCCCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 1129
QY 61 GAATCTGAGAGACGAGGAGCCCTTGTGCTTGTGGCCAGAAATGCTGC 104
Db 1130 GAATCTGAGAGACGAGGAGCCCTTGTGCTTGTGGCCAGAAATGCTGC 1173

RESULT 13
AAZ20983 standard; DNA; 2270 BP.
XX AC AAZ20983;
XX DT 30-NOV-1999 (first entry)
XX DE Chimeric nucleic acid -706TNFpGB3'UTR.
XX KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW KW psoriasis; graft versus host disease; lupus erythematosus;
KW KW diabetes; ankylosing spondylitis; rheumatoid arthritis; promoter; ds.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT promoter 7..733
FT FT /*tag= a
FT FT /label= TNFalpha_promoter
FT FT /note= "Human TNFalpha native promoter (AAZ20973)"
FT FT 740..1477
FT FT /*tag= b
FT FT /product= "Truncated Granzyme B"
FT FT /note= "Inactivating dipeptide absent"
FT FT 1490..2264
FT FT /*tag= c
FT FT /label= TNFalpha_3'UTR
XX PN WO9943840-A1.
XX PD 02-SEP-1999.
```

XX PF 12-JAN-1999; 99WO-US00637.
XX PR 27-FEB-1998; 98US-0076316.
XX PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX PI Tatake RJ, Marlin SD, Barton RW;
XX DR WPI; 1999-527630/44.
XX PT A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
XX promoter and an apoptosis-inducing Granzyme B polynucleotide -
PS Claim 4; Fig 12; 71pp; English.
XX CC This sequence represents chimeric nucleic acid -706TNFpGB3'UTR. This
CC comprises at least one TNFalpha (tumour necrosis factor alpha) promoter
CC enhancer region (AAZ20975-Z20978), a TNFalpha native promoter (AAZ20973),
CC a DNA encoding a truncated form of the apoptosis-inducing Granzyme B
CC protein (AAZ20982), and a TNFalpha 3'UTR (untranslated region)
CC sequence (AAZ20979). TNFalpha is one of a number of cytokines
CC produced by inflammatory cells. Upregulation and/or dysregulation
CC of cytokines in inflamed tissue may be directly or indirectly
CC responsible for exacerbation of chronic inflammatory diseases.
CC Introduction of this chimeric nucleotide to activated inflammatory cells
CC causes them to undergo apoptosis. Pharmaceutical compositions of this
CC chimeric nucleotide may be useful for treating inflammatory disorders
CC such as multiple sclerosis, Crohn's disease, ulcerative colitis,
CC psoriasis, graft versus host disease, lupus erythematosus,
CC insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis,
CC and in particular, rheumatoid arthritis. The use of such chimeric
CC nucleotides offers simpler and cheaper long-term relief, in comparison
CC with existing conventional pharmaceutical and invasive surgery methods.
XX SQ Sequence 2270 BP; 556 A; 647 C; 545 G; 522 T; 0 other;
Query Match 100.0%; Score 104; DB 20; Length 2270;
Best Local Similarity 100.0%; Pred. No. 2.8e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTGTGATCCCTGACATCTG 60
DB 1705 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTGTGATCCCTGACATCTG 1764
QY 61 GAATCTGAGACCAAGGAGCCCTTGTGCTGCGCCAGATGCTGC 104
DB 1765 GAATCTGAGACCAAGGAGCCCTTGTGCTGCGCCAGATGCTGC 1808
RESULT 14
AAZ20984
ID AAZ20984 standard; DNA; 2570 BP.
XX AC AAZ20984;
XX DT 30-NOV-1999 (first entry)
XX DE Chimeric nucleic acid -1005TNFpGB3'UTR.
XX TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW psoriasis; graft versus host disease; lupus erythematosus;
KW diabetes; ankylosing spondylitis; rheumatoid arthritis; promoter; ds.
XX OS Synthetic.
OS Homo sapiens.
XX FH Key Location/Qualifiers
FH promoter 7..1033
FT /*tag= a
FT /label= TNFalpha_promoter
FT /note= "Human TNFalpha native promoter (AAZ20973)"

FT CDS 1040..1777
FT /*tag= b
FT /product= "Truncated Granzyme B"
FT /note= "Inactivating dipeptide absent"
FT 3'UTR 1790..2564
FT /*tag= c
FT /label= TNFalpha_3'UTR
XX PN WO9943840-A1.
XX PD 02-SEP-1999.
XX PF 12-JAN-1999; 99WO-US00637.
XX PR 27-FEB-1998; 98US-0076316.
XX PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX PI Tatake RJ, Marlin SD, Barton RW;
XX DR WPI; 1999-527630/44.
XX PT A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
XX promoter and an apoptosis-inducing Granzyme B polynucleotide -
PS Claim 4; Fig 13; 71pp; English.
XX CC This sequence represents chimeric nucleic acid -1005TNFpGB3'UTR. This
CC comprises at least one TNFalpha (tumour necrosis factor alpha) promoter
CC enhancer region (AAZ20975-Z20978), a TNFalpha native promoter (AAZ20973),
CC a DNA encoding a truncated form of the apoptosis-inducing Granzyme B
CC protein (AAZ20982), and a TNFalpha 3'UTR (untranslated region)
CC sequence (AAZ20979). TNFalpha is one of a number of cytokines
CC produced by inflammatory cells. Upregulation and/or dysregulation
CC of cytokines in inflamed tissue may be directly or indirectly
CC responsible for exacerbation of chronic inflammatory diseases.
CC Introduction of this chimeric nucleotide to activated inflammatory cells
CC causes them to undergo apoptosis. Pharmaceutical compositions of this
CC chimeric nucleotide may be useful for treating inflammatory disorders
CC such as multiple sclerosis, Crohn's disease, ulcerative colitis,
CC psoriasis, graft versus host disease, lupus erythematosus,
CC insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis,
CC and in particular, rheumatoid arthritis. The use of such chimeric
CC nucleotides offers simpler and cheaper long-term relief, in comparison
CC with existing conventional pharmaceutical and invasive surgery methods.
XX SQ Sequence 2570 BP; 639 A; 711 C; 650 G; 570 T; 0 other;
Query Match 100.0%; Score 104; DB 20; Length 2570;
Best Local Similarity 100.0%; Pred. No. 2.8e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTGTGATCCCTGACATCTG 60
DB 2005 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTGTGATCCCTGACATCTG 2064
QY 61 GAATCTGAGACCAAGGAGCCCTTGTGCTGCGCCAGATGCTGC 104
DB 2065 GAATCTGAGACCAAGGAGCCCTTGTGCTGCGCCAGATGCTGC 2108
RESULT 15
AAV39005
ID AAV39005 standard; DNA; 3634 BP.
XX AC AAV39005;
XX DT 23-SEP-1998 (first entry)
XX DE TNF-alpha gene used in the course of the invention.
XX TNF-alpha; alteration; immunoreactivity; human cell;
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;

KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO9826061-A2.
XX
PD 18-JUN-1998.
XX
PF 08-DEC-1997; 97WO-US22740.
XX
PR 01-DEC-1997; 97US-0982272.
PR 09-DEC-1996; 96US-0032145.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cantwell M, Kipps TJ, Sharma S;
XX
DR WPI; 1998-348521/30.
XX
PT Vectors containing accessory molecule ligand genes - used for
PT altering immunoreactivity of cells, particularly for treatment of
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX
PS Disclosure; Pages 107-108; 167pp; English.
XX
CC The present sequence represents a TNF-alpha gene. The sequence is
CC used to exemplify the method of the invention. The specification
CC describes a method for altering the immunoreactivity of human cells
CC which comprises introducing a gene encoding an accessory molecule
CC ligand (AML) into the cells so that the AML is expressed on the surface
CC of the cells. Vectors containing the AML genes can be used in gene
CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid
CC arthritis. They can also be used for vaccination to produce immunity
CC against a virus cell, bacteria, protein, fungus or neoplasia.
XX
SQ Sequence 3634 BP; 906 A; 959 C; 975 G; 794 T; 0 other;

Query Match 100.0%; Score 104; DB 19; Length 3634;
Best Local Similarity 100.0%; Pred. No. 3.1e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGCGGCTTACAGCTTTGATCCCTGACATCTG 60
DB 2808 GAATTCAAACTGGGGCTCCAGAACTCACTGCGGCTTACAGCTTTGATCCCTGACATCTG 2867

QY 61 GAATCTGGAGACCGAGGAGCCTTTGGTCTCTGGCCAGAAATGCTGC 104
DB 2868 GAATCTGGAGACCGAGGAGCCTTTGGTCTCTGGCCAGAAATGCTGC 2911

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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2188.293 Million cell updates/sec

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Perfect score: 104
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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30: em_htg_hum:*
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33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	400	11 G13533	G13533 SHGC-11076
2	104	100.0	1275	6 I08430	I08430 Sequence 5
3	104	100.0	1323	6 I07953	I07953 Sequence 6
4	104	100.0	1324	6 E00702	E00702 cDNA encod1
5	104	100.0	1324	6 I03610	I03610 Sequence 2
6	104	100.0	1465	6 I04244	I04244 Sequence 2
7	104	100.0	1585	6 A37272	A37272 Sequence 12
8	104	100.0	1585	6 I04169	I04169 Sequence 1
9	104	100.0	1585	6 I04198	I04198 Sequence 1
10	104	100.0	1585	6 I08384	I08384 Sequence 5
11	104	100.0	1585	6 I08429	I08429 Sequence 3
12	104	100.0	1585	9 HUMTNFAA	M10988 Human tumor
13	104	100.0	1606	6 I07541	I07541 Sequence 22
14	104	100.0	1643	6 ARI46199	ARI46199 Sequence
15	104	100.0	1676	9 HSTNFR	X01394 Human mRNA
16	104	100.0	3103	9 HUMTNFX	BC028148 Homo sapi
17	104	100.0	3634	6 ARI00270	M26331 Human tumor
18	104	100.0	3634	6 ARI49925	ARI00270 Sequence
19	104	100.0	3634	9 HSTNFA	ARI49925 Sequence
20	104	100.0	4830	9 AY066019	X02910 Human gene
21	104	100.0	7112	6 AX100950	AY066019 Homo sapi
22	104	100.0	7112	6 AX100965	AX100950 Sequence
23	104	100.0	7112	9 HUMTNFAB	AX100965 Sequence
24	104	100.0	817	6 E02109	M16441 Human tumor
25	104	100.0	817	9 HSTNFBX	Z15026 Homo sapien
26	104	100.0	81800	9 HSTNFBX	Y14768 Homo sapien
27	104	100.0	100000	9 AP000505	AP000505 Homo sapi
28	104	100.0	135784	9 AL662847	AL662847 Human DNA
29	104	100.0	139399	9 AL662801	AF129756 Homo sapi
30	104	100.0	184666	9 DJ201G24	AP000899 Homo sapi
31	104	100.0	212055	2 AP000899	A16444 Xho-PstI fr
32	102.4	98.5	817	6 A16444	E02109 DNA sequenc
33	102.4	98.5	817	6 E02109	AJ249755 Homo sapi
34	102.4	98.5	1047	9 HSA249755	M35592 Synthetic h
35	102.4	98.5	1379	12 SYNNTFTRP	I08863 Sequence 3
36	102.4	98.5	1560	6 I08863	AF019963 Paplo ham
37	73	70.2	1459	9 AF019963	AX344556 Sequence
38	59.8	57.5	349980	6 AX344556	AX344556 Sequence
39	58.2	56.0	349980	6 AX344568	AX344568 Sequence
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41	49.6	47.7	2610	4 HRTNFA	M64087 Equus cabal
42	40.4	38.8	3200	4 RABTNF	M12846 Rabbit tumo
43	40.4	38.8	6577	4 RABTNF	M60340 Rabbit lymf
44	35	33.7	209882	2 AC103554	AC103554 Rattus no
45	34.8	33.5	1071	10 CPV77036	U77036 Cavia porce

ALIGNMENTS

RESULT 1
G13533
LOCUS G13533 400 bp DNA linear STS 30-MAR-2000
DEFINITION SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G13533
VERSION G13533.1 GI:1129272
KEYWORDS STS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Olivier, M., and Cox, D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)

COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: oliviereshgc.stanford.edu
Primer A: CACTAGAATCAACTGGGGC
Primer B: GAGGAAGCCCTAAGTCCAC
STS size: 166
PCR profile:
Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs derived from M10988 -- Unigene.

FEATURES
source location/Qualifiers
1.400
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6"
/clone_lib="Human"

STS
primer_bind 210..375
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BASE COUNT 104 a 120 c 87 g 89 t
ORIGIN

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Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCTGACATCTG 60
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Db 216 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCTGACATCTG 275

QY 61 GAATCTGGAGACCAAGGAGCCCTTGGTCTGGCCAGAATGCTGC 104
|||||
Db 276 GAATCTGGAGACCAAGGAGCCCTTGGTCTGGCCAGAATGCTGC 319

RESULT 2
LOCUS 108430 1275 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 8604606.
ACCESSION 108430
VERSION 108430.1 GI:5888860

KEYWORDS
SOURCE
ORGANISM

Unknown.
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
TITLE CYSTEINE-DEPLETED MUTAINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
JOURNAL NECROSIS FACTOR PROTEINS
Patent: WO 8604606-A 5 14-AUG-1986;

FEATURES

source

Location/Qualifiers
1..1275
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BASE COUNT 297 a 357 c 309 g 312 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1275;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCTGACATCTG 60
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Db 693 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCTGACATCTG 752

QY 61 GAATCTGGAGACCAAGGAGCCCTTGGTCTGGCCAGAATGCTGC 104
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Db 753 GAATCTGGAGACCAAGGAGCCCTTGGTCTGGCCAGAATGCTGC 796

RESULT 3

LOCUS 107953 1323 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 6 from Patent EP 0168214.
ACCESSION 107953
VERSION 107953.1 GI:5893335

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 1323)
AUTHORS Aggarwal,B.B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.
TITLE Tumor necrosis factor, methods for its preparation, compositions containing it, DNA encoding it and assay method using such DNA
JOURNAL Patent: EP 0168214-A2 6 15-JAN-1986;

FEATURES
source location/Qualifiers
1..1323
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ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1323;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCTGACATCTG 60
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Db 750 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCTGACATCTG 809

QY 61 GAATCTGGAGACCAAGGAGCCCTTGGTCTGGCCAGAATGCTGC 104
|||||
Db 810 GAATCTGGAGACCAAGGAGCCCTTGGTCTGGCCAGAATGCTGC 853

RESULT 4

LOCUS E00702 1324 bp RNA linear PAT 29-SEP-1997
DEFINITION CDNA encoding human tumor necrosis factor.
ACCESSION E00702
VERSION E00702.1 GI:2168979
KEYWORDS JP 1986040221-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1324)
AUTHORS Baraa,B.A., Debilsudo,B.G., San,H.R. and Guren,E.N.
TITLE TUMOR NECROTIC FACTOR
JOURNAL Patent: JP 1986040221-A 1 26-FEB-1986;

COMMENT

GENENTECH INC
OS homosapiens
PN JP 1986040221-A/1
PD 26-FEB-1986
PF 05-JUL-1985 JP 1985149075

PR 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 628059, PR
05-JUL-1984 US 84 628060, 03-DEC-1984 US 84 677156, PR
03-DEC-1984 US 84 677257, 03-DEC-1984 US 84 677454, PI BARAA
BUSHIYAN AGAMARU, DEBITSU DO BANNOOMAN GETSUDERU, PI SAN HII RII,
PI GUREN EBAN NEDOUIN
PC A61K35/12, A61K35/02, A61K35/14, A61K37/04, A61K37/04, C07H21/02,
PC C07H21/04,
PC C12N15/00;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: cell_type=promyelocytes;
CC *source: cell_line=HL-60;
CC *source: clone=lambda42-4, lambda16-4;
FH key location/Qualifiers
FT sig_peptide <1.61
FT mat_peptide 62.532
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FT <1.535 /product='tumor necrosis factor' FT CDS
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FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 298 a 387 c 308 g 331 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAATCTGAGAGACGAGGAGCCTTGTGTTCTGGCCAGAATGCTGC 104
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DB 811 GAATCTGAGAGACGAGGAGCCTTGTGTTCTGGCCAGAATGCTGC 854

RESULT 5
LOCUS I03610 1324 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4650674.
ACCESSION I03610
VERSION I03610.1 GI:268632
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1324)
AUTHORS Aggarwal, B.B. and Lee, S.He.
TITLE Synergistic cytotoxic composition
JOURNAL Patent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco, CA
FEATURES
source location/Qualifiers
1.1324
/organism="unknown"
BASE COUNT 298 a 387 c 308 g 331 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 60
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DB 751 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 810

QY 61 GAATCTGAGAGACGAGGAGCCTTGTGTTCTGGCCAGAATGCTGC 104

DB 811 GAATCTGAGAGACGAGGAGCCTTGTGTTCTGGCCAGAATGCTGC 854
|||||

RESULT 6
LOCUS I04244 1465 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4677197.
ACCESSION I04244
VERSION I04244.1 GI:268725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1465)
AUTHORS Lin, L.S. and Yamamoto, R.
TITLE Purification method for tumor necrosis factor
JOURNAL Patent: US 4677197-A 2 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
source location/Qualifiers
1.1465
/organism="unknown"
BASE COUNT 324 a 429 c 363 g 349 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1465;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 883 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 942

QY 61 GAATCTGAGAGACGAGGAGCCTTGTGTTCTGGCCAGAATGCTGC 104
|||||
DB 943 GAATCTGAGAGACGAGGAGCCTTGTGTTCTGGCCAGAATGCTGC 986

RESULT 7
LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 12 from Patent WO9404196.
ACCESSION A37272
VERSION A37272.1 GI:2294369
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Ville, R.G. and Hart, I.R.
TITLE TUMOUR THERAPY
JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;
IMP CANCER RES TECH (GB)
FEATURES
source location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

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Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGAGACGAGGAGCCTTGTGTTCTGGCCAGAATGCTGC 104
|||||
DB 1063 GAATCTGAGAGACGAGGAGCCTTGTGTTCTGGCCAGAATGCTGC 1106

RESULT 8
LOCUS I04169 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677063.
ACCESSION I04169
VERSION I04169.1 GI:268716
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van Arsdell,J.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677063-A 1 30-JUN-1987;
FEATURES
source location/Qualifiers
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BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. NO. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 1003 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACGAGGAGCCCTTGTGCTCGGCCAGATGCTGC 104
|||||
Db 1063 GAATCTGAGACGAGGAGCCCTTGTGCTCGGCCAGATGCTGC 1106

RESULT 9
LOCUS I04198 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677064.
ACCESSION I04198
VERSION I04198.1 GI:268719
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Van Arsdell,J.N. and Lin,L.S.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677064-A 1 30-JUN-1987;
FEATURES
source location/Qualifiers
1..1585
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

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Best Local Similarity 100.0%; Pred. NO. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAATCTGAGACGAGGAGCCCTTGTGCTCGGCCAGATGCTGC 104
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Db 1063 GAATCTGAGACGAGGAGCCCTTGTGCTCGGCCAGATGCTGC 1106

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LOCUS I08384 1585 bp DNA linear PAT 02-DEC-1994

DEFINITION Sequence 5 from Patent WO 8602381.
ACCESSION I08384
VERSION I08384.1 GI:588904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van Arsdell,J.N.
TITLE HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8602381-A 5 24-APR-1986;
FEATURES
source location/Qualifiers
1..1585
BASE COUNT 352 a 473 c 389 g 371 t
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DEFINITION Sequence 3 from Patent WO 8604606.
ACCESSION I08429
VERSION I08429.1 GI:588859
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
TITLE CYSTEINE-DEPLETED MUTAINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR NECROSIS FACTOR PROTEINS
JOURNAL Patent: WO 8604606-A 3 14-AUG-1986;
FEATURES
source location/Qualifiers
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BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

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Best Local Similarity 100.0%; Pred. NO. 4.3e-25;
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DEFINITION Human tumor necrosis factor (TNF) mRNA.
ACCESSION M10988
VERSION M10988.1 GI:339737
KEYWORDS
SOURCE Human cDNA to mRNA, clone pE4.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Wang,A.M., Creasey,A.A., Ladner,M.B., Lin,L.S., Strickler,J., Van
Arsdell,J.N., Yamamoto,R. and Mark,D.F.
TITLE Molecular cloning of the complementary DNA for human tumor necrosis
factor
JOURNAL Science 228 (4696), 149-154 (1985)
MEDLINE 85142190
PUBMED 3856324
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source Location/Qualifiers
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DEFINITION Sequence 22 from Patent EP 0313104.
ACCESSION 107541
VERSION 107541.1 GI:590445
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1606)
AUTHORS Fiers,W.C., Franssen,L.M., Tavernier,J.H.L., Marmernout,A.L.M., van
der Heyden,J., Allet,B. and Kawahima,E.H.
TITLE Purification, production and use of tumor necrosis factors
JOURNAL Patent: EP 0313104-A2 22 26-APR-1989;
FEATURES
source Location/Qualifiers
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BASE COUNT 357 a 494 c 394 g 361 t
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Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1135 GAATCTGAGAGACGAGCGCTTGTGCTTGCGCCAGAAATGCTGC 1178
RESULT 14
LOCUS AR146199 1643 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 36 from patent US 6218179.
ACCESSION AR146199
VERSION AR146199.1 GI:15109388
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1643)
AUTHORS Webster,K.A., Bishopric,N.H., Murphy,B., Laderoute,K.R. and
Green,C.J.
TITLE Tissue specific hypoxia regulated constructs
JOURNAL Patent: US 6218179-A 36 17-APR-2001;
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source Location/Qualifiers
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DEFINITION Human mRNA for tumor necrosis factor.
ACCESSION X01394
VERSION X01394.1 GI:37219
KEYWORDS tumor necrosis factor.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1643)
AUTHORS Pennica,D., Nedwin,G.E., Hayflick,J.S., Seedburg,P.H., Derynck,R.,
Palladino,M.A., Kohr,W.J., Aggarwal,B.B. and Goeddel,D.V.
TITLE Human tumour necrosis factor: precursor structure, expression and
homology to lymphotoxin
JOURNAL Nature 312 (5996), 724-729 (1984)
MEDLINE 85086244
PUBMED 6392892
REFERENCE 2 (bases 1 to 1643)
AUTHORS Shirai,T., Yamaguchi,H., Ito,H., Todd,C.W. and Wallace,R.B.
TITLE Cloning and expression in Escherichia coli of the gene for human
tumour necrosis factor
JOURNAL Nature 313 (6005), 803-806 (1985)
MEDLINE 85137898
PUBMED 3883195
COMMENT In the genomic sequence from ref [2] the mature protein starts with
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FEATURES
source Location/Qualifiers
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VSYOTKVNLLSAIKSPCQRETFEGAEAKPWEPYILGGVFQLEKGDRLSAEINRPDYL
DFAESGQVYFGIIAL"
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/product="mature TNF (aa 1-157)"
misc_feature 1630. .1635
/note="put. polyadenylation signal"
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-801-371A-1

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	104	100.0	1643	4 US-09-505-250-4	Sequence 4, Appl
3	104	100.0	3634	3 US-09-166-186-1	Sequence 1, Appl
4	104	100.0	3634	4 US-09-313-932-1	Sequence 1, Appl
5	104	100.0	3634	4 US-09-109-663-34	Sequence 34, Appl
6	28	26.9	28720	4 US-09-341-587-7	Sequence 7, Appl
7	26.4	25.4	3181	1 US-08-655-086-1	Sequence 1, Appl
8	25.8	24.8	3889	4 US-09-484-970B-39	Sequence 39, Appl
9	25.8	24.8	4031	1 US-08-159-784-1	Sequence 1, Appl
10	25.6	24.6	642	4 US-09-328-111-82	Sequence 82, Appl
11	25.6	24.6	2634	3 US-08-911-853-30	Sequence 30, Appl
12	25.6	24.6	2634	4 US-09-479-409-30	Sequence 30, Appl
13	25.6	24.6	2634	4 US-09-479-453-30	Sequence 30, Appl
14	25.6	24.6	17612	3 US-08-911-853-29	Sequence 29, Appl
15	25.6	24.6	17612	4 US-09-479-409-29	Sequence 29, Appl
16	25.6	24.6	17612	4 US-09-479-453-29	Sequence 29, Appl
17	25.4	24.4	220	4 US-09-263-933-22	Sequence 22, Appl
18	25.4	24.4	604	4 US-09-068-880-1	Sequence 1, Appl
19	25.4	24.4	1026	4 US-09-068-880-14	Sequence 14, Appl
20	25.4	24.4	1289	4 US-09-247-155-138	Sequence 138, App
21	25.4	24.4	1467	4 US-09-330-317B-17	Sequence 17, Appl
22	25.4	24.4	1467	4 US-09-808-589A-17	Sequence 17, Appl
23	25.4	24.4	1956	3 US-08-867-352-20	Sequence 20, Appl
24	25.4	24.4	4145	1 US-08-314-917-1	Sequence 1, Appl
25	25.4	24.4	4145	1 US-08-265-046-1	Sequence 1, Appl
26	25.4	24.4	4145	2 US-08-465-522-1	Sequence 1, Appl
27	25.4	24.4	4145	5 PCT-US93-11401-1	Sequence 1, Appl

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30	25.4	24.4	4951	4 US-09-707-802-1	Sequence 1, Appl
31	25.4	24.4	4951	4 US-09-991-326-1	Sequence 1, Appl
32	25.4	24.4	7076	4 US-09-837-863-20	Sequence 20, Appl
33	25.4	24.4	7076	4 US-09-837-863-21	Sequence 21, Appl
34	25.4	24.4	7092	4 US-09-837-863-19	Sequence 19, Appl
35	25.4	24.4	7092	4 US-09-837-863-22	Sequence 22, Appl
36	25.4	24.4	7208	3 US-09-166-186-107	Sequence 107, App
37	25.4	24.4	7208	4 US-09-313-932-107	Sequence 107, App
38	25.4	24.4	7573	4 US-09-837-863-27	Sequence 27, Appl
39	25.4	24.4	8299	1 US-08-462-014-2	Sequence 2, Appl
40	25.4	24.4	8299	3 US-08-923-137-3	Sequence 3, Appl
41	25.4	24.4	8299	4 US-08-973-334-5	Sequence 5, Appl
42	25.4	24.4	8299	4 US-09-563-869A-5	Sequence 5, Appl
43	25.4	24.4	13910	4 US-09-263-933-1	Sequence 1, Appl
44	25.4	24.4	13910	4 US-09-263-933-8	Sequence 8, Appl
45	25.4	24.4	13910	4 US-09-263-933-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
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; ANTI-SENSE: NO
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RESULT 2

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US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
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RESULT 3

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US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- $\alpha$  EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
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; ORGANISM: Homo sapiens
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; NAME/KEY: Intron
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; LOCATION: (1870)..(2070)
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; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
; TITLE: homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
; US-09-166-186-1
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RESULT 4

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; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- $\alpha$ 
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
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; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes:
; TITLE: structure, homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
; US-09-313-932-1

Query Match          100.0%; Score 104; DB 4; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTGTGATCCCTGACATCTG 60
        |||
DB      2808 GAATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTGTGATCCCTGACATCTG 2867

QY      61 GAATCTGAGACGAGGAGCCCTTGTCTGCGCCAGATGCTGC 104
        |||
DB      2868 GAATCTGAGACGAGGAGCCCTTGTCTGCGCCAGATGCTGC 2911

RESULT 5
US-09-109-663-34
; Sequence 34, Application us/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
; APPLICANT: Tu, Guang-Chou
; APPLICANT: Israel, Yedy
; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
; TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 9855-301
```

```
; CURRENT APPLICATION NUMBER: US/09/109,663
; CURRENT FILING DATE: 1998-07-03
; EARLIER APPLICATION NUMBER: 60/051,705
; EARLIER FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TNF(alpha) cDNA
; US-09-109-663-34

Query Match          100.0%; Score 104; DB 4; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTGTGATCCCTGACATCTG 60
        |||
DB      2808 GAATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTGTGATCCCTGACATCTG 2867

QY      61 GAATCTGAGACGAGGAGCCCTTGTCTGCGCCAGATGCTGC 104
        |||
DB      2868 GAATCTGAGACGAGGAGCCCTTGTCTGCGCCAGATGCTGC 2911

RESULT 6
US-09-341-587-7/c
; Sequence 7, Application us/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain
; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 28720
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-341-587-7

Query Match          26.9%; Score 28; DB 4; Length 28720;
Best Local Similarity 58.3%; Pred. No. 3;
Matches 49; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY      2 AATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTGTGATCCCTGACATCTG 61
        |||
DB      14762 AATTCAGAGGGCTCTAGAGAGAGAGAGGGGACATCTCCATTTGACAGGCTCTCAGG 14703

QY      62 AATCTGAGACGAGGAGCCCTTGTG 85
        |||
DB      14702 TATTTGTGACAGGAATCATCTG 14679

RESULT 7
US-08-655-086-1
; Sequence 1, Application us/08655086
; Patent No. 5821089
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOTT A.
; APPLICANT: BUECHTER, DOUGLAS
; APPLICANT: ZHANG, GUANGHUI
; APPLICANT: CONNOLLY, KEVIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DILMORTH & BARESE
; STREET: 333 EARLE OVINGTON BOULEVARD
```

CITY: UNIONDALE
STATE: NY
COUNTRY: US
ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,086
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S.
REGISTRATION NUMBER: 32,063
REFERENCE/DOCKET NUMBER: 203-1632
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-228-8484
TELEFAX: 516-228-8516
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-655-086-1

Query Match 25.4%; Score 26.4; DB 1; Length 3181;
Best Local Similarity 57.1%; Pred. No. 5.5;
Matches 48; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 8 AACTGGGCTCCAGACTCACTGGGCTTACAGCTTGATCCCTGACATCTGGAATCTG 67
DB 1317 AGCGAGGTGTCCCGGACCCCTGGCGCTGTGCTCTGTGCGCAAGATGAGAGGCTG 1376
QY 68 GAGACCAGGAGCCTTGTGTTCTG 91
DB 1377 GAGCTCAGGAGCCCTTGCCCTG 1400

RESULT 8
US-09-484-970B-39/c
Sequence 39, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 39
LENGTH: 3889
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 251277.1CB1
US-09-484-970B-39

Query Match 24.8%; Score 25.8; DB 4; Length 3889;
Best Local Similarity 60.9%; Pred. No. 9.4;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 30 TGGGGCTTACACTTGTATCCCTGACATCTGGAATCTGAGAGCCAGGAGCCTTGTGTTCTC 89
DB 625 TGGCCCTGTGCGCAGTTCCTGACCCCATGAGCCAGCGAGACACTGCGTCTTGTGTTCTC 566

QY 90 TGGCCAGAA 98
DB 565 CGGTCAGCA 557

RESULT 9
US-08-159-784-1
Sequence 1, Application US/08159784
Patent No. 5643783
GENERAL INFORMATION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00246/170001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4031
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-159-784-1

Query Match 24.8%; Score 25.8; DB 1; Length 4031;
Best Local Similarity 54.8%; Pred. No. 9.6;
Matches 51; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 11 TGGGCTCCAGACTCACTGGGCTTACAGCTTGATCCCTGACATCTGGAATCTGAG 70
DB 2513 TGGCCACACTGGGCCACACGAGGCAATTCCTGACCTCTTCCACTGGAAGCGAAA 2572
QY 71 ACCAGGAGCCTTGTGTTCTGCGCAGATGCTG 103
DB 2573 TGAAGGGGACAGGAGACCGAGCGATGCTG 2605

RESULT 10
US-09-328-111-82/c
Sequence 82, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.

```

; APPLICANT: Dertl, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-82

```

Query Match	24.6%	Score 25.6;	DB 4;	Length 642;
Best Local Similarity	87.58;	Pred. No. 6.3;		
Matches	28; Conservative	0; Mismatches	4; Indels	0; Gaps

Oy 47 ATCCCTGACATCTGGAACTCGAGAGACCAGGA 78
||| ||||||||| | | |||||
Db 413 ATCACTGACATCTGGAATCTGACAACAAGGA 382

RESULT 11
US-08-911-853-30/c
; Sequence 30, Application US/08911853
; Patent No. 6048710

```

; GENERAL INFORMATION:
;
; APPLICANT: Gerritse, Gijlsbert
;
; APPLICANT: Quax, Wilhelmus J.
;
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
;
; TITLE OF INVENTION: EXPRESSION LEVELS
;
; NUMBER OF SEQUENCES: 37
;
; CORRESPONDENCE ADDRESS:
;

```

;
; ADDRESS: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
;

```

; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE

```

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

```

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; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0.0
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```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,853
;

```

```

; FILING DATE:
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: 08/699,092
FILING DATE: 16-AUG-1996

ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 00000

REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620

TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 30:

```

; SEQUENCE CHARACTERISTICS:
;     LENGTH: 2634 base pairs

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
;

```

```

;          TOPOLOGY: 1linear
US-08-911-853-30

```

Query Match 24.68; Score 25.6; DB 3; Length 2634;

Best Local Similarity	54.28;	Pred. No. 9.8;
Matches	52; Conservative	0; Mismatches
		44; Indels
		0; Gaps
		0;

QY 8 AACCTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTGTATCCCTGCATCTGGAAATCTG 67
| | | | | | | | | | | | | | | | | |
DB 317 ACCTCGGGCCCTGTCATCTCGGGCGGAGAGGGTTGAACCAAGACAGGTCGAAGTCC 258

```

QY      68  GAGACCAAGGAGCCTTGGTCTCTGGCCAGATGCTG 103
          ||| | | | | | | | | | | | | | | |
Db      257  TCGACCTGGGCGCGGATGCTTCGGCCAGTGGCG 222

```

RESULT 12
US-09-479-409-30/c
; Sequence 30, Application US/09479409

```

; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gtjsbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
;

```

STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94304-1013

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

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;
;
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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; SOFTWARE: FastSEO for Windows Version 2.0
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/09/479,409
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853

ATTORNEY/AGENT INFORMATION:

NAME: Claister, Debra J
REGISTRATION NUMBER: 33-888

REFERENCE/DOCKET NUMBER: GC361-2

TELEPHONE: 650-846-7622
TELEFAX: 650-845-6504

TELEFAX: 850-845-0504
; INFORMATION FOR SEQ ID NO: 30:
SEQUENCE AND RESTRICTION

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs

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```
; nucleic acid
; TYPE:
; STRANDEDNESS: single
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US-09-479-409-30

Query Match	24.68;	Score 25.6;	DB 4;	Length 2634;
Best Local Similarity	54.28;	Pred. No. 9.8;		
Matches 52; Conservative	0;	Mismatches 44;	Indels 0;	Gaps 0;

```

oy      8 AACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAACTCG 67
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
db     317 ACCTCGGGCGCCTGTGCATCTCGCGCGGGAAGGGGTGAACCCAGACAGTCAGATCC 258

```

```

qy      68 GAGACCAGGAGCCTTTGTTCTGGCCAGAAATGCTG 103
        ||| ||| || ||| ||||| |||
Db      257 TCGACCTGGGGCGGATGCTTTCGGCCAGGTGGCG 222

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RESULT 13
US-09-479-453-30/c
: Sequence 30, Application US/09479453

; Patent No. 6313283
; GENERAL INFORMATION:

APPLICANT: Gerritse, Gijshert
APPLICANT: Quax, Wilhelmus J..
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,453
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Glatster, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-479-453-30

```

RESULT 14
; US-08-911-853-29/c
; Sequence 29, Application US/08911853
; Patent No. 6048710
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gjsbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

```

```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/911,853
:
: FILING DATE:
:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/699,092
: FILING DATE: 16-AUG-1996
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Glaister, Debra J
: REGISTRATION NUMBER: 33,888
: REFERENCE/DOCKET NUMBER: GC361-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-846-7620
: TELEFAX: 650-846-6504
:
: INFORMATION FOR SEQ ID NO: 29:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 17612 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-911-853-29

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	Query Match	24.68;	Score 25.6;	DB 3;	Length 17612;	
	Best Local Similarity	54.2%;	Pred. No. 18;			
	Matches 52;	Conservative	0;	Mismatches 44;	Indels 0;	Gaps 0;
QY	8 AACTGGGCGCTCCAGAACTCACTGGGGCGCTACAGCCTTGATCCCTGACATCTGAATCTG 67 					
Dd	4732 ACCTCGGGCGCCTGTGCATCTCGGCGCGAAGGGTTGAACCAGACAGTTCGAAGTCC 46733 					
QY	68 GAGACCAGGAGGCCCTTTGGTCTCTGGCCAGAATGCTG 103 					
Dd	4672 TCGACCTGGGGCGCGATGCTTTCCGGCCAAGTGGCCG 4637 . 					

RESULT 15
 US-09-479-409-29/c
 ; Sequence 29, Application US/09479409
 ; Patent No. 6225106
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT: Gerritse, Gtjsbert
 ;
 APPLICANT: Quax, Wilhelmus J.
 ;
 TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 ;
 TITLE OF INVENTION: EXPRESSION LEVELS
 ;
 NUMBER OF SEQUENCES: 37
 ;
 CORRESPONDENCE ADDRESS:
 ;
 ADDRESSEE: Genencor International
 ;
 STREET: 925 Page Mill Road
 ;
 CITY: Palo Alto
 ;
 STATE: CA
 ;
 COUNTRY: USA
 ;
 ZIP: 94304-1013
 ;
 COMPUTER READABLE FORM:
 ;
 MEDIUM TYPE: Diskette
 ;
 COMPUTER: IBM Compatible
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 OPERATING SYSTEM: DOS
 ;
 SOFTWARE: FastSeq for windows Version 2.0
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 CURRENT APPLICATION DATA:
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 APPLICATION NUMBER: US/09/479,409
 ;
 FILING DATE:
 ;
 PRIOR APPLICATION DATA:
 ;
 APPLICATION NUMBER: 08/911,853
 ;
 FILING DATE:
 ;
 ATTORNEY/AGENT INFORMATION:
 ;
 NAME: Gjalster, Debra J
 ;
 REGISTRATION NUMBER: 33,888
 ;
 REFERENCE/DOCKET NUMBER: GC361-2
 ;
 TELECOMMUNICATION INFORMATION:
 ;
 TELEPHONE: 650-846-7620
 ;
 TELEFAX: 650-845-6504
 ;
 INFORMATION FOR SEQ ID NO: 29:
 ;
 SEQUENCE CHARACTERISTICS:
 ;
 LENGTH: 17612 base pairs
 ;
 TYPE: nucleic acid
 ;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:48:50 ; Search time 137.252 Seconds
(without alignments)
1124.814 Million cell updates/sec

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Perfect score: 104
Sequence: 1 gaattcaactggggcctcc.....ggtctgccaagaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1055720 seqs, 742224136 residues

Total number of hits satisfying chosen parameters: 2111440

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	104	100.0	104	9	US-09-801-371A-1	Sequence 1, Appl1
2	104	100.0	104	9	US-09-801-371A-5	Sequence 5, Appl1
3	104	100.0	1643	9	US-10-218-547-3	Sequence 3, Appl1
4	104	100.0	1643	9	US-10-272-411-4	Sequence 4, Appl1
5	104	100.0	1643	9	US-10-272-328A-4	Sequence 4, Appl1
6	104	100.0	3634	9	US-09-824-322B-1	Sequence 1, Appl1
7	104	100.0	3634	9	US-09-932-300-34	Sequence 34, Appl1
8	77	74.0	81	9	US-09-801-371A-7	Sequence 7, Appl1
9	50	48.1	50	9	US-09-801-371A-8	Sequence 8, Appl1
10	43	41.3	43	9	US-09-801-371A-2	Sequence 2, Appl1
11	43	41.3	43	9	US-09-801-371A-6	Sequence 6, Appl1
12	42	40.4	418	9	US-09-796-692-6223	Sequence 6223, Ap
13	42	40.4	418	9	US-10-040-862-6223	Sequence 6223, Ap
14	33	31.7	51	9	US-09-801-371A-10	Sequence 10, Appl1
15	27.4	26.3	3617	10	US-09-874-069-2	Sequence 2, Appl1
16	27.4	26.3	116592	10	US-09-818-512-3	Sequence 3, Appl1
17	27.2	26.2	122186	9	US-09-563-728A-36	Sequence 36, Appl1
18	26.8	25.8	2894	9	US-10-225-567A-669	Sequence 669, App
19	26.8	25.8	3117	10	US-09-963-766-2	Sequence 2, Appl1

c	20	26.8	25.8	5340	10	US-09-963-766-5	Sequence 5, Appl1
c	21	26.8	25.8	74868	9	US-10-175-523-67	Sequence 67, Appl
c	22	26.6	25.6	223	10	US-09-783-590-6687	Sequence 6687, Ap
c	23	26.6	25.6	496	10	US-09-783-590-4240	Sequence 4240, Ap
c	24	26.4	25.4	3347	9	US-10-000-773A-16	Sequence 16, Appl
c	25	26.4	25.4	4409	9	US-10-216-705-22	Sequence 22, Appl
c	26	26.4	25.4	6728	9	US-10-060-036-136	Sequence 136, App
c	27	26.4	25.4	6728	9	US-10-171-311-35	Sequence 35, Appl
c	28	26.4	25.4	6728	9	US-10-149-352-1	Sequence 1, Appl1
c	29	26.4	25.4	6728	10	US-09-954-456-782	Sequence 782, App
c	30	26.4	25.4	6728	10	US-09-880-107-3946	Sequence 3946, Ap
c	31	26.4	25.4	6753	9	US-10-198-846-13252	Sequence 13252, A
c	32	26.4	25.4	6769	9	US-10-198-846-13897	Sequence 13897, A
c	33	26.2	25.2	2650	9	US-10-106-698-2090	Sequence 2090, Ap
c	34	26	25.0	1836	9	US-09-738-626-2125	Sequence 2125, Ap
c	35	26	25.0	26048	9	US-10-091-504-1556	Sequence 1556, Ap
c	36	26	25.0	26048	10	US-09-764-869-1556	Sequence 1556, Ap
c	37	26	25.0	3309400	9	US-09-738-626-1	Sequence 1, Appl1
c	38	25.8	24.8	210	9	US-09-104-750-3	Sequence 3, Appl1
c	39	25.8	24.8	488	10	US-09-864-761-10140	Sequence 10140, A
c	40	25.8	24.8	488	10	US-09-783-590-848	Sequence 848, App
c	41	25.8	24.8	603	9	US-10-092-154-1031	Sequence 1031, Ap
c	42	25.8	24.8	603	10	US-09-764-847-1031	Sequence 1031, Ap
c	43	25.8	24.8	717	10	US-09-764-877-3941	Sequence 3941, Ap
c	44	25.8	24.8	3506	9	US-09-104-750-24	Sequence 24, Appl
c	45	25.8	24.8	4005	10	US-09-349-015-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801, 371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

Query Match 100.0%; Score 104; DB 9; Length 104;
Best local similarity 100.0%; Pred. No. 6.8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGAAGAGCCAGGAGCCCTTGGTCTGCGCAGATGCTGC 60
DB 1 GAATTCGAAGAGCCAGGAGCCCTTGGTCTGCGCAGATGCTGC 60

QY 61 GAATTCGAAGAGCCAGGAGCCCTTGGTCTGCGCAGATGCTGC 104
DB 61 GAATTCGAAGAGCCAGGAGCCCTTGGTCTGCGCAGATGCTGC 104

RESULT 2
US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:

```
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5
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```
Query Match          100.0%; Score 104; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GAATCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTACAGCTTGATCCCTGACATCTG 60
          |||||||
Db      104 GAATCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTACAGCTTGATCCCTGACATCTG 45
QY      61 GAATCTGAGACGACGAGGAGCCCTTGCTTGCTGCGCCAGAATGCTGC 104
          |||||||
Db      44 GAATCTGAGACGACGAGGAGCCCTTGCTTGCTGCGCCAGAATGCTGC 1
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RESULT 3

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US-10-218-547-3
; Sequence 3, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-218-547-3
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Query Match          100.0%; Score 104; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GAATCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTACAGCTTGATCCCTGACATCTG 60
          |||||||
Db      1070 GAATCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTACAGCTTGATCCCTGACATCTG 1129
QY      61 GAATCTGAGACGACGAGGAGCCCTTGCTTGCTGCGCCAGAATGCTGC 104
          |||||||
Db      1130 GAATCTGAGACGACGAGGAGCCCTTGCTTGCTGCGCCAGAATGCTGC 1173
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RESULT 4

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US-10-272-411-4
; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
```

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; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4
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Query Match          100.0%; Score 104; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GAATCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTACAGCTTGATCCCTGACATCTG 60
          |||||||
Db      1070 GAATCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTACAGCTTGATCCCTGACATCTG 1129
QY      61 GAATCTGAGACGACGAGGAGCCCTTGCTTGCTGCGCCAGAATGCTGC 104
          |||||||
Db      1130 GAATCTGAGACGACGAGGAGCCCTTGCTTGCTGCGCCAGAATGCTGC 1173
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RESULT 5

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US-10-272-328A-4
; Sequence 4, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-328A-4
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Query Match          100.0%; Score 104; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 1070 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGAGACACGAGGAGCCCTTGGTCTCTGGCCAGAATGCTGC 104
|||||
Db 1130 GAATCTGAGACACGAGGAGCCCTTGGTCTCTGGCCAGAATGCTGC 1173

RESULT 6

US-09-824-322B-1
; Sequence 1, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shaahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA
; FILE REFERENCE: ISPH-0501
; CURRENT APPLICATION NUMBER: US/09/824,322B
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 09/313,932
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: US 09/166,186
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; NAME/KEY: exon
; LOCATION: (615)..(981)
; NAME/KEY: Intron
; LOCATION: (982)..(1588)
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; NAME/KEY: Intron
; LOCATION: (1635)..(1821)
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; NAME/KEY: Intron
; LOCATION: (1870)..(2070)
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology and
; TITLE: chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-824-322B-1

Query Match 100.0%; Score 104; DB 9; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 2808 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 2867

QY 61 GAATCTGAGACACGAGGAGCCCTTGGTCTCTGGCCAGAATGCTGC 104
|||||
Db 2868 GAATCTGAGACACGAGGAGCCCTTGGTCTCTGGCCAGAATGCTGC 2911

RESULT 7

US-09-932-300-34
; Sequence 34, Application US/09932300
; Publication No. US20030032788A1
; GENERAL INFORMATION:
; APPLICANT: GARVER, Eric
; APPLICANT: TU, Guang-Chou
; APPLICANT: ISRAEL, Yedy
; TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION
; FILE REFERENCE: 9855-302
; CURRENT APPLICATION NUMBER: US/09/932,300
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/051,705
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 09/109,663
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-932-300-34

Query Match 100.0%; Score 104; DB 9; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 2808 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 2867

QY 61 GAATCTGAGACACGAGGAGCCCTTGGTCTCTGGCCAGAATGCTGC 104
|||||
Db 2868 GAATCTGAGACACGAGGAGCCCTTGGTCTCTGGCCAGAATGCTGC 2911

RESULT 8

US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 7
; LENGTH: 81
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-7

Query Match 74.0%; Score 77; DB 9; Length 81;
Best Local Similarity 79.2%; Pred. No. 3.1e-18;

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Matches 61; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTGTGATCCTGACATCTG 60
Db 5 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTGTGATCCTGACATCTG 64
QY 61 GAATCTGAGAGACGAGG 77
Db 65 GAATCTGAGAGACGAGG 81

RESULT 9
US-09-801-371A-8
; Sequence 8, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-8

Query Match
Best Local Similarity 48.1%; Score 50; DB 9; Length 50;
Matches 39; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTGTGATC 50
Db 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTGTGATC 50

RESULT 10
US-09-801-371A-2
; Sequence 2, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-2

Query Match
Best Local Similarity 41.3%; Score 43; DB 9; Length 43;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTTGTGAT 47
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Db 1 TCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTTGTGAT 43

RESULT 11
US-09-801-371A-6/c
; Sequence 6, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-6

Query Match
Best Local Similarity 41.3%; Score 43; DB 9; Length 43;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTTGTGAT 47
Db 43 TCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTTGTGAT 47
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RESULT 12
US-09-796-692-6223
; Sequence 6223, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
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; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6223
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)
; OTHER INFORMATION: n-A,T,C or G
US-09-796-692-6223

Query Match
  Query Match      40.4%; Score 42; DB 9; Length 418;
  Best Local Similarity 90.0%; Pred. No. 1.4e-05;
  Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY      1 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGATCC 50
Db      326 GAATCAAACTGGGGCTTCCAGACTCACTGGGGCTTACAGCTTGATCC 375

RESULT 13
US-10-040-862-6223
; Sequence 6223, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6223
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)
; OTHER INFORMATION: n-A,T,C or G
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US-10-040-862-6223

Query Match
  Query Match      40.4%; Score 42; DB 9; Length 418;
  Best Local Similarity 90.0%; Pred. No. 1.4e-05;
  Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY      1 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGATCC 50
Db      326 GAATCAAACTGGGGCTTCCAGACTCACTGGGGCTTACAGCTTGATCC 375

RESULT 14
US-09-801-371a-10
; Sequence 10, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 51
; TYPE: RNA
; ORGANISM: Oryctolagus cuniculus
US-09-801-371a-10

Query Match
  Query Match      31.7%; Score 33; DB 9; Length 51;
  Best Local Similarity 70.7%; Pred. No. 0.017;
  Matches 29; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY      1 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAG 41
Db      1 GCAUUCAAACUGAGGCUUCCAGACUCACUGGGCCUUCAG 41

RESULT 15
US-09-874-069-2/c
; Sequence 2, Application US/09874069
; Patent No. US20020064826A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Cytokine Receptor-like Polynucleotides, Polypeptides, and Anti
; FILE REFERENCE: PT021P1
; CURRENT APPLICATION NUMBER: US/09/874,069
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US00/32525
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,621
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-874-069-2

Query Match
  Query Match      26.3%; Score 27.4; DB 10; Length 3617;
  Best Local Similarity 57.6%; Pred. No. 3.3;
  Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY      20 CAGAACTCACTGGGGCTTACAGCTTGATCCCTGACATCTGAATCTGAGACGAG 79
Db      969 CTGAACCTGCTGTGCGCAATGTCATGTGTGCGCTTCACTCGGAACCTGTAGAGACGTGAAG 910
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Wed Jul 2 12:18:21 2003

Qy 80 CCTTGGTTCTGGCCAGAATGCTGC 104
|| || || || || || || ||
Db 909 GGCTTCAGCCCTGTGCCACAATGAAGC 885

Search completed: July 1, 2003, 22:16:13
Job time : 142.252 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 19:55:04 ; Search time 571.871 Seconds
(without alignments)
2188.293 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaaatggggcctccagaa.....actggggcctacagcttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
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7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
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28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rod: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	43	100.0	400	11	G13533	G13533 SHGC-11076
2	43	100.0	817	6	A16444	A16444 Xho-PstI fr
3	43	100.0	817	6	E02109	E02109 DNA sequence
4	43	100.0	1047	9	HS249755	AJ249755 Homo sapi
5	43	100.0	1275	6	I08430	I08430 Sequence 5
6	43	100.0	1323	6	I07953	I07953 Sequence 6
7	43	100.0	1324	6	E00702	E00702 cDNA encod1
8	43	100.0	1324	6	I03610	I03610 Sequence 2
9	43	100.0	1379	12	SYNTNFTRP	M3592 Synthetic h
10	43	100.0	1465	6	I04244	I04244 Sequence 2
11	43	100.0	1560	6	I08863	I08863 Sequence 3
12	43	100.0	1585	6	A37272	A37272 Sequence 12
13	43	100.0	1585	6	I04169	I04169 Sequence 1
14	43	100.0	1585	6	I04198	I04198 Sequence 1
15	43	100.0	1585	6	I08384	I08384 Sequence 5
16	43	100.0	1585	6	I08429	I08429 Sequence 3
17	43	100.0	1585	9	HUMTNFAA	M10988 Human tumor
18	43	100.0	1606	6	I07541	I07541 Sequence 22
19	43	100.0	1643	6	ARI46199	ARI46199 Sequence
20	43	100.0	1643	9	HSTNFR	X01394 Human mRNA
21	43	100.0	1676	9	BC028148	BC028148 Homo sapi
22	43	100.0	3103	9	HUMTNFX	M26331 Human tumor
23	43	100.0	3634	6	ARI00270	ARI00270 Sequence
24	43	100.0	3634	6	ARI49925	ARI49925 Sequence
25	43	100.0	3634	9	HSTNFA	X02910 Human gene
26	43	100.0	4830	9	AY066019	AY066019 Homo sapi
27	43	100.0	7112	6	AX100950	AX100950 Sequence
28	43	100.0	7112	6	AX100965	AX100965 Sequence
29	43	100.0	7112	9	HUMTNFAB	M16441 Human tumor
30	43	100.0	16310	9	HSTNFBAB	Z15026 Homo sapien
31	43	100.0	81800	9	HSY14768	Y14768 Homo sapien
32	43	100.0	100000	9	AP000505	AP000505 Homo sapi
33	43	100.0	135784	9	AL662847	AL662847 Human DNA
34	43	100.0	139399	9	AL662801	AL662801 Human DNA
35	43	100.0	184666	9	DJ201624	AF129756 Homo sapi
36	43	100.0	212055	2	AP000899	AP000899 Homo sapi
37	38.4	89.3	1459	9	AF019963	AF019963 Papio ham
38	34	79.1	2610	4	HRSTNFA	M64087 Equus cabal
39	30.6	71.2	1671	4	RABTNFM	M12845 Rabbit tumo
40	30.6	71.2	3200	4	RABTNF	M12846 Rabbit tumo
41	30.6	71.2	6577	4	RABTNFB	M60340 Rabbit lym
42	27.8	64.7	4349	4	AF011927	AF011927 Bos indic
43	27.8	64.7	4352	4	AF011926	AF011926 Bos tauru
44	27.4	63.7	177917	9	AC025824	AC025824 Homo sapi
45	27.4	63.7	186254	2	AC091544	AC091544 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS G13533 400 bp DNA STS 30-MAR-2000
DEFINITION SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G13533
VERSION G13533.1 GI:1129272
KEYWORDS STS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Olivier, M. and Cox, D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)

COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: oliviereshgc.stanford.edu
Primer A: CACTAGAATTCAACTGGGGC
Primer B: GAGGAGGCGCTAAGTCCAC
STS size: 166
PCR profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

FEATURES

Prepared with primer pairs derived from M10988 -- Unigene.
Location/Qualifiers
1..400

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6"

/clone_11b="Human"

STS
primer_bind 210..375

primer_bind 210..231

BASE COUNT 104 a 120 c 87 g 89 t

ORIGIN

Query Match

100.0%; Score 43; DB 11; Length 400;

Best Local Similarity 100.0%; Pred. No. 3.9e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTACCTGAGCTTTGA 43

|||||

DB 220 TCAAACTGGGGCTCCAGAACTCACTACCTGAGCTTTGA 262

RESULT 2

LOCUS

A16444 817 bp DNA linear PAT 05-OCT-1994

DEFINITION Xho-PstI fragment from THP-1 cells.

ACCESSION A16444

VERSION A16444.1 GI:641014

KEYWORDS

SOURCE Homo sapiens.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 817)

AUTHORS Soma,G.I., Mizuno,D., Tsuji,Y. and Kobayashi,N.

TITLE Anti-aids preparation

JOURNAL Patent: EP 0450240-A 9 09-OCT-1991;

Location/Qualifiers
1..817

FEATURES
source /organism="Homo sapiens"

BASE COUNT 183 a 268 c 206 g 160 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 817;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGAGCTTTGA 43

|||||

DB 716 TCAAACTGGGGCTCCAGAACTCACTGAGCTTTGA 758

RESULT 3

LOCUS

E02109 817 bp DNA linear PAT 29-SEP-1997

DEFINITION DNA sequence coding for anti-tumor polypeptide.

ACCESSION

E02109.1 GI:2170351

VERSION

KEYWORDS JP 1989256390-A/1.

UNIDENTIFIED.

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 817)

Soma,G., Mizuno,D. and Tsuji,Y.

NOVEL DNA AND PRODUCTION THEREOF, NOVEL PLASMID HAVING SAME, NOVEL

POLYPEPTIDE AND PRODUCTION THEREOF AND NOVEL ANTINEOPLASTIC AGENT

PATENT: JP 1989256390-A 1 12-OCT-1989;

SOMA GENICHIRO, MIZUNO DENICHI

PN JP 1989256390-A/1

COMMENT

PD 12-OCT-1989

PF 03-APR-1988 JP 1988081683

PI SOMA GENICHIRO, MIZUNO DENICHI, TSUJI YOSHIKI PC

C12N15/00,A61K37/24,C07K13/00,C12P21/02,(C12P21/02,C12R1:19); CC

strandedness: Double;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

*source: library=THP-1 cell;

key location/Qualifiers

FT

mat_peptide >1..<817

/product="Anti-tumor polypeptide".

FEATURES

source

1..817
/organism="Glycine max"
/db_xref="taxon:3847"

BASE COUNT 183 a 268 c 206 g 160 t

ORIGIN

Query Match

100.0%; Score 43; DB 6; Length 817;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGAGCTTTGA 43

|||||

DB 716 TCAAACTGGGGCTCCAGAACTCACTGAGCTTTGA 758

RESULT 4

LOCUS

HSA249755 1047 bp DNA linear PRI 29-SEP-1999

DEFINITION Homo sapiens TNF-alpha gene for tumor necrosis factor-alpha, 3'

UTR, country United Arab Emirates.

ACCESSION AJ249755

VERSION AJ249755.1 GI:6002308

KEYWORDS TNF-alpha gene; tumor necrosis factor-alpha.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1047)
AUTHORS Farhan,A.J., Pravica,V. and Hutchinson,I.V.
TITLE Identification of new rare variant of human TNF-alpha 3' UTR
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Farhan,A.J.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1999) Farhan A.J., CID-Immunology Research Division, Manchester University, Medical School, Stopford Building, Oxford Road, Manchester, M13 9PT, UNITED KINGDOM

FEATURES
source
1..1047
/organism="Homo sapiens"
/db_xref="taxon:9606"
/country="United Arab Emirates"
/note="new rare variant"
1..1047
/gene="TNF-alpha"
1..>1047
/gene="TNF-alpha"
322
variation
/gene="TNF-alpha"
/replace="t"

BASE COUNT 260 a 282 c 221 g 284 t
ORIGIN

Query Match 100.0%; Score 43; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 225 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 267

RESULT 5
LOCUS I08430 1275 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 8604606.
ACCESSION I08430
VERSION I08430.1 GI:588860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
TITLE CYSTEINE-DEPLETED MUTAINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR NECROSIS FACTOR PROTEINS
JOURNAL Patent: WO 8604606-A 5 14-AUG-1986;
FEATURES
source
1..1275
/organism="unknown"

BASE COUNT 297 a 357 c 309 g 312 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1275;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 697 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 739

RESULT 6
LOCUS I07953 1323 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 6 from Patent EP 0168214.
ACCESSION I07953
VERSION I07953.1 GI:589335

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1323)
AUTHORS Aggarwal,B.B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.
TITLE Tumor necrosis factor, methods for its preparation, compositions containing it, DNA encoding it and assay method using such DNA
JOURNAL Patent: EP 0168214-A2 6 15-JAN-1986;
FEATURES
source
1..1323
/organism="unknown"

BASE COUNT 298 a 387 c 308 g 330 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1323;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 754 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 796

RESULT 7
LOCUS E00702 1324 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding human tumor necrosis factor.
ACCESSION E00702
VERSION E00702.1 GI:2168979
KEYWORDS
SOURCE JP 1986040221-A/1.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1324)
AUTHORS Baraa,B.A., Debitsudo,B.G., San,H.R. and Guren,E.N.
TITLE TUMOR NECROTIC FACTOR
JOURNAL Patent: JP 1986040221-A 1 26-FEB-1986;
COMMENT
OS homomapslens
PN JP 1986040221-A/1
PD 26-FEB-1986
PF 05-JUL-1985 JP 1985149075
PR 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 628059, PR
05-JUL-1984 US 84 628060, 03-DEC-1984 US 84 677156, PR
03-DEC-1984 US 84 677257, 03-DEC-1984 US 84 677454 PI BARAA
BUSHIYAN AGAMARU, DEBITSUDO BANNOOMAN GETSUDERU, PI SAN HIR RII,
PI GUREN EBAN NEDOUIN
PC A61K35/12,A61K35/02,A61K35/14,A61K35/74,A61K37/04,C07H21/02,
PC C07H21/04,
PC C12N15/00;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: cell_type=promyelocytes;
CC *source: cell_line=HL-60;
CC *source: clone=lamda42-4, lamda16-4;
FH Key location/Qualifiers
FT sig_peptide <1..61
FT mat_peptide 62..532
FT /product='tumor necrosis factor' FT CDS
FT <1..535 /product='tumor necrosis factor' FT 3'UTR

536..>1324.
location/Qualifiers
1..1324
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 298 a 387 c 308 g 331 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 43
|||||
755 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 797

Db

RESULT 8

LOCUS I03610 1324 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4650674.
ACCESSION I03610
VERSION I03610.1 GI:268632
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1324)
AUTHORS Aggarwal,B.B. and Lee,S.He.
TITLE Synergistic cytotoxic composition
JOURNAL Patent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco, CA

FEATURES
source 1..1324
/organism="unknown"

BASE COUNT 298 a 387 c 308 g 331 t

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 43
|||||
755 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 797

Db

RESULT 9

LOCUS SYNNTNTRP 1379 bp mRNA linear SYN 27-APR-1993
DEFINITION Synthetic human tumor necrosis factor mRNA, complete cds.
ACCESSION M35592
VERSION M35592.1 GI:209485
KEYWORDS tumor necrosis factor.
SOURCE Altered human leukemic B-cell line Ball-1, cDNA to mRNA, clone PM324-346.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1379)
AUTHORS Nobuhara,M., Kanamori,T., Nagase,Y., Nii,A., Morishita,H.,
Tohyama,J., Andoh,S. and Kurimoto,M.
TITLE The expression of human tumor necrosis factor in E. coli
JOURNAL Nucleic Acids Symp. Ser. 17, 131-134 (1986)
MEDLINE 87174864
PUBMED 3031624

FEATURES
source Location/Qualifiers
1..1379
/organism="synthetic construct"
/db_xref="taxon:32630"
178..879
/note="synthetic tumor necrosis factor precursor"
/codon_start=1
/transl_table=11
/protein_id="AAC42098.1"
/db_xref="GI:209486"
/translation="MSTESMRDVELAEALPKKTGGPGSRCLFLSLFSLIVAGA
TTLFCLLHFGVMGPQREEFPRDLISPLAQAVRSSRTPSDKPAHVAVANPQAEGL
QWLNRANALLANGVELRDNLVYPSEGLYLYSQVLEFRGCGCPSTHVLTHTISRIA
VSIQTKNLLSAIKSPCQRETEPGAEPWYEPITLGVFQLEKGDRLSAEINRPDYL
DFAESGVYFGIIL"

CDS

sig_peptide 178..399
mat_peptide 400..876
/note="synthetic tumor necrosis factor signal peptide"
/product="synthetic tumor necrosis factor"

BASE COUNT 318 a 438 c 336 g 287 t

ORIGIN

Query Match 100.0%; Score 43; DB 12; Length 1379;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 43
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Db 1100 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 1142

Db

RESULT 10

LOCUS I04244 1465 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4677197.
ACCESSION I04244
VERSION I04244.1 GI:268725
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1465)
AUTHORS Lin,L.S. and Yamamoto,R.
TITLE Purification method for tumor necrosis factor
JOURNAL Patent: US 4677197-A 2 30-JUN-1987;
Cetus Corporation; Emeryville, CA

FEATURES
source 1..1465
/organism="unknown"

BASE COUNT 324 a 429 c 363 g 349 t

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1465;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 43
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Db 887 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 929

Db

RESULT 11

LOCUS I08863 1560 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent WO 8806625.
ACCESSION I08863
VERSION I08863.1 GI:588416
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1560)
AUTHORS Mark,D.F., Lin,L.S., Thomson,J.W. and Yamamoto,R.
TITLE ARGININE-DEPLETED HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8806625-A 3 07-SEP-1988;
MEDLINE
PUBMED

FEATURES
source Location/Qualifiers
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/organism="unknown"

BASE COUNT 340 a 473 c 381 g 366 t

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 1049

Db

RESULT 12
A37272
LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 12 from Patent WO9404196.
ACCESSION A37272
VERSION A37272.1 GI:2294369
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Ville,R.G. and Hart,I.R.
TITLE TUMOUR THERAPY
JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;
IMP CANCER RES TECH (GB)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32644"
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 13
I04169
LOCUS I04169 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677063.
ACCESSION I04169
VERSION I04169.1 GI:268716
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677063-A 1 30-JUN-1987;
FEATURES
source Location/Qualifiers
1.1585
/organism="unknown"
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 14
I04198
LOCUS I04198 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677064.
ACCESSION I04198
VERSION I04198.1 GI:268719
KEYWORDS
SOURCE unknown.
ORGANISM unknown.

Unclassified.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Van Arsdell,J.N.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677064-A 1 30-JUN-1987;
FEATURES
source Location/Qualifiers
1.1585
/organism="unknown"
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 15
I08384
LOCUS I08384 1585 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 8602381.
ACCESSION I08384
VERSION I08384.1 GI:588904
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
TITLE HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8602381-A 5 24-APR-1986;
FEATURES
source Location/Qualifiers
1.1585
/organism="unknown"
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

Search completed: July 1, 2003, 21:27:27
Job time : 572.871 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 18:32:14 ; Search time 99.1633 Seconds
(without alignments)
976.530 Million cell updates/sec

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Perfect score: 43

Sequence: 1 tcaactgggcccctccagaa.....actgggcctacagcttga 43

Scoring table:

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	43	21	AAZ99817
2	43	100.0	50	21	AAZ99815
3	43	100.0	104	21	AAZ99816
4	43	100.0	787	20	AAZ20979
5	43	100.0	815	8	AAAT70075
6	43	100.0	817	11	AAQ04340
7	43	100.0	818	10	AAAT91035
8	43	100.0	1200	8	AAAT70072
9	43	100.0	1200	10	AAAT90969

10	43	100.0	1275	7	AAAT60558	Sequence encoding
11	43	100.0	1323	7	AAAT60363	Sequence encoding
12	43	100.0	1324	21	AAAT21085	Human low adenosin
13	43	100.0	1324	21	AAA34963	Human adenosine re
14	43	100.0	1560	9	AAAT80219	Sequence of pE4 en
15	43	100.0	1585	7	AAAT60557	Sequence encoding
16	43	100.0	1585	7	AAAT60527	Sequence encoding
17	43	100.0	1606	7	AAAT60446	Sequence encoding
18	43	100.0	1606	17	AAAT15424	Human tumour necro
19	43	100.0	1643	8	AAAT71307	Sequence encoding
20	43	100.0	1643	17	AAAT31021	Human tumour necro
21	43	100.0	1643	24	ABK13195	Human tumour necro
22	43	100.0	2270	20	AAZ20983	Chimeric nucleic a
23	43	100.0	2570	20	AAZ20984	TNF-alpha gene use
24	43	100.0	3634	19	AAAT39005	Tumour necrosis fa
25	43	100.0	3634	20	AAAT09014	Tumour necrosis fa
26	43	100.0	3634	21	AAAT63770	Human TNF-alpha ge
27	43	100.0	3634	21	AAA40760	Human tumour necro
28	43	100.0	7112	22	AAAT86085	Lymphotoxin and tu
29	43	100.0	7112	22	AAAT57450	Human tumour necro
30	43	100.0	16310	21	AAAT21086	Human low adenosin
31	43	100.0	16310	21	AAA34964	Human adenosine re
32	43	100.0	17634	21	AAAT21087	Human low adenosin
33	43	100.0	17634	21	AAAT21087	Human low adenosin
34	43	100.0	17634	21	AAA34965	Human adenosine re
35	43	100.0	17634	21	AAA34965	Human adenosine re
36	43	100.0	81800	24	ABK84756	Human CDNA differe
37	41.4	96.3	1585	15	AAQ58037	Tumour necrosis fac
38	30.6	71.2	51	21	AAZ99916	Sequence of the st
39	24.6	57.2	811	13	AAQ22830	Sequence encoding
40	24.6	57.2	1678	13	AAQ22829	Sequence encoding
41	22.2	51.6	27	21	AAZ99917	Sequence of the st
42	22.2	51.6	2834	22	AAAT3215	Human immune/haema
43	22.2	51.6	2834	22	AAAT3218	Human immune/haema
44	22.2	51.6	109906	24	ABK94411	DNA encoding endot
45	21.4	49.8	1274	19	AAAT34215	Human secreted pro

ALIGNMENTS

RESULT 1	
AAZ99817	
ID	AAZ99817 standard; RNA; 43 BP.
XX	
AC	AAZ99817;
XX	
DT	12-JUL-2000 (first entry)
XX	
DE	Cis-acting nucleotide sequence derived from human TNF-alpha.
XX	
KW	Cis-acting sequence; Intron removal; trans-acting factor; alpha-subunit;
KW	RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW	tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200014255-A1.
XX	
PD	16-MAR-2000.
XX	
PF	06-SEP-1999; 99WO-IL00483.
XX	
PR	07-SEP-1998; 98IL-0126112.
PR	26-OCT-1998; 98IL-0126757.
XX	
PA	(YISS) YISSUM RES & DEV CO.
XX	
PI	Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX	
DR	WPI; 2000-257000/22.
XX	
PT	Regulation of gene expression by mRNA splicing is carried out using a

PT cis-acting nucleotide sequence controlled by phosphorylation of the
PT alpha-subunit of eukaryotic initiation factor 2 -
XX
PS Claim 5; Page 15; 75pp; English.
XX
CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a
CC gene which harbours at least one cis-acting nucleotide sequence. This
CC removal is effected during the production of mRNA of the gene, and
CC depends on activation of a trans-acting factor which is an RNA-activated
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can
CC be used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a cis-acting nucleotide sequence of the
CC invention.
XX
SQ Sequence 43 BP; 10 A; 13 C; 11 G; 9 T; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCTCCAGACTCACTGGGCTACAGCTTGA 43
XX
Db 1 TCAAACTGGGGCTCCAGACTCACTGGGCTACAGCTTGA 43

RESULT 2
AAZ99815
ID AAZ99815 standard; RNA; 50 BP.
XX
AC AAZ99815;
XX
DT 12-JUL-2000 (first entry)
XX
DE Sequence of the stem loop of tumour necrosis factor-alpha gene.
XX
KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200014255-A1.
XX
PD 16-MAR-2000.
XX
PF 06-SEP-1999; 99WO-IL00483.
XX
PR 07-SEP-1998; 98IL-0126112.
PR 26-OCT-1998; 98IL-0126757.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX
DR WPI; 2000-257000/22.
XX
PT Regulation of gene expression by mRNA splicing is carried out using a
PT cis-acting nucleotide sequence controlled by phosphorylation of the
PT alpha-subunit of eukaryotic initiation factor 2 -
XX
PS Example 7; Fig 5B; 75pp; English.
XX
CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a

CC gene which harbours at least one cis-acting nucleotide sequence. This
CC removal is effected during the production of mRNA of the gene, and
CC depends on activation of a trans-acting factor which is an RNA-activated
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can
CC be used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a fragment of the 3'UTR of human TNF-alpha.
XX
SQ Sequence 50 BP; 12 A; 15 C; 12 G; 11 U; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 50;
Best Local Similarity 79.1%; Pred. No. 1.6e-07;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCTCCAGACTCACTGGGCTACAGCTTGA 43
XX
Db 5 UCAAACTGGGGCTCCAGAACUCACUGGGCCUACAGCUUGA 47

RESULT 3
AAZ99816
ID AAZ99816 standard; RNA; 104 BP.
XX
AC AAZ99816;
XX
DT 12-JUL-2000 (first entry)
XX
DE Cis-acting nucleotide sequence derived from human TNF-alpha.
XX
KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200014255-A1.
XX
PD 16-MAR-2000.
XX
PF 06-SEP-1999; 99WO-IL00483.
XX
PR 07-SEP-1998; 98IL-0126112.
PR 26-OCT-1998; 98IL-0126757.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX
DR WPI; 2000-257000/22.
XX
PT Regulation of gene expression by mRNA splicing is carried out using a
PT cis-acting nucleotide sequence controlled by phosphorylation of the
PT alpha-subunit of eukaryotic initiation factor 2 -
XX
PS Claim 4; Page 15; 75pp; English.
XX
CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a
CC gene which harbours at least one cis-acting nucleotide sequence. This
CC removal is effected during the production of mRNA of the gene, and
CC depends on activation of a trans-acting factor which is an RNA-activated
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the

CC level of RNA-activated protein kinase (PKR) activity. The sequence can
CC be used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a cis-acting nucleotide sequence of the
CC invention.
XX
SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGCTACAGCTTTGA 43
|||||
DB 5 TCAAACTGGGGCCTCCAGAACTCACTGGGCTACAGCTTTGA 47

RESULT 4
AAZ20979
ID AAZ20979 standard; DNA; 787 BP.
XX
AC AAZ20979;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human TNFalpha 3'UTR.
XX
KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW psoriasis; graft versus host disease; lupus erythematosus;
KW diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
XX
OS Homo sapiens.
XX
PN WO9943840-A1.
XX
PD 02-SEP-1999.
XX
PF 12-JAN-1999; 99WO-US00637.
XX
PR 27-FEB-1998; 98US-0076316.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Tatake RJ, Marlin SD, Barton RW;
XX
DR WPI; 1999-527630/44.
XX
CC This sequence represents a human TNFalpha (tumour necrosis factor alpha)
CC 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984)
CC were constructed comprising at least one TNFalpha promoter enhancer
CC region (AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA
CC encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a
CC TNFalpha 3'UTR sequence. TNFalpha is one of a number of
CC cytokines produced by inflammatory cells. Upregulation and/or
CC dysregulation of cytokines in inflamed tissue may be directly or
CC indirectly responsible for exacerbation of chronic inflammatory
CC diseases. Introduction of the chimeric nucleotide to activated
CC inflammatory cells causes them to undergo apoptosis. Pharmaceutical
CC compositions of the chimeric nucleotide may be useful for treating
CC inflammatory disorders such as multiple sclerosis, Crohn's disease,
CC ulcerative colitis, psoriasis, graft versus host disease, lupus
CC erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing
CC spondylitis, and in particular, rheumatoid arthritis. The use of such
CC chimeric nucleotides offers simpler and cheaper long-term relief, in
CC comparison with existing conventional pharmaceutical and invasive surgery

CC methods.
XX
SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 other;

Query Match 100.0%; Score 43; DB 20; Length 787;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGCTACAGCTTTGA 43
|||||
DB 226 TCAAACTGGGGCCTCCAGAACTCACTGGGCTACAGCTTTGA 268

RESULT 5
AAN70075
ID AAN70075 standard; DNA; 815 BP.
XX
AC AAN70075;
XX
DT 20-JAN-1991 (first entry)
XX
DE Human anti-tumor polypeptide xho-PstI fragment.
XX
KW Anti-tumor; cancer; cytotoxic; ss.
XX
OS Homo sapiens.
XX
PN EP247906-A.
XX
PD 02-DEC-1987.
XX
PF 04-FEB-1987; 87EP-0400261.
XX
PR 17-JUL-1986; 86JP-0169522.
PR 04-FEB-1986; 86JP-0021302.
XX
PA (MIZU/) MIZUNO D.
XX
PI Mizuno D;
PI Soma GI;
XX
DR WPI; 1987-336540/48.
XX
DT Anti-tumor polypeptides - prepared using recombinant DNA prepared
PT from genomic DNA of human acute leukemia cell THP-1.
XX
PS Disclosure; Fig 7; 63pp; English.
XX
CC The sequence is an xho-PstI fragment of an anti-tumor protein.
CC The polypeptide is cytotoxic to human tumor cells but not to normal
CC cells. They are also cytotoxic to primary cell cultures obtained
CC from metastasis lesions of patients suffering from striated muscle
CC tumors. They are also resistant to all chemotherapeutic agents.
CC See also AAN70073-74, AAP70077-78 and AAP95592.
XX
SQ Sequence 815 BP; 183 A; 267 C; 205 G; 160 T; 0 other;

Query Match 100.0%; Score 43; DB 8; Length 815;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGCTACAGCTTTGA 43
|||||
DB 716 TCAAACTGGGGCCTCCAGAACTCACTGGGCTACAGCTTTGA 758

RESULT 6
AAQ04340
ID AAQ04340 standard; DNA; 817 BP.
XX
AC AAQ04340;
XX
DT 21-SEP-1990 (first entry)

XX THP-1.
DE Acute leukaemia cell; THP-1; anti-tumour agent; ss.
XX Homo sapiens.
OS JP02088598-A.
XX
XX 28-MAY-1990.
PD
XX 22-SEP-1988; 88JP-0239154.
XX
XX 22-SEP-1988; 88JP-0239154.
XX
XX (SOMA/) SOMA G.
XX
XX WPI; 1990-143138/19.
DR
XX Intrinsic TNF prodn. derivation agents - contain primer and trigger,
PT at least one of which has TNF activity.
XX
XX Disclosure; ; P; Japanese.
XX
XX Used in the prodn. of TNF prodn. agents.
XX
XX Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 other;
SQ
Query Match 100.0%; Score 43; DB 11; Length 817;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 716 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 758
RESULT 7
AAN91035
ID AAN91035 standard; DNA; 818 BP.
XX
AC AAN91035;
XX
XX 11-MAR-1990 (first entry)
DT
XX XhoI - PstI section of gene for anti-cancer peptide.
DE
XX Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
KM
XX THP-1 cells.
OS
XX JF01095784-A.
PN
XX 13-APR-1989.
PD
XX 06-OCT-1987; 87JP-0252174.
PF
XX 06-OCT-1987; 87JP-0252174.
XX
XX 06-OCT-1987; 87JP-0252174.
PR
XX (SENG/) SEN G.
XX
XX WPI; 1989-154899/21.
DR
XX Novel DNA, plasmid and polypeptide(s)
PT - useful as anticarcinogenic agents
XX
XX Fig 3; ; 17pp; Japanese.
PS
XX Section of gene for anticarcinogenic peptide. It is genomic DNA or cDNA
CC from THP-1 cells.
XX
XX Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 other;
SQ

Query Match 100.0%; Score 43; DB 10; Length 818;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 717 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 759
RESULT 8
AAN70072
ID AAN70072 standard; DNA; 1200 BP.
XX
XX AAN70072;
AC
XX 20-JAN-1991 (first entry)
DT
XX Human anti-tumor polypeptide.
DE
XX Anti-tumor; cancer; cytotoxic; ss.
XX
XX Homo sapiens.
OS
XX EP247906-A.
PN
XX 02-DEC-1987.
PD
XX 04-FEB-1987; 87EP-0400261.
PF
XX 17-JUL-1986; 86JP-0169522.
PR
XX 04-FEB-1986; 86JP-0021302.
XX
XX (MIZU/) MIZUNO D.
PA
XX Mizuno D;
PI Soma GI;
PI
XX WPI; 1987-336540/48.
DR
XX Anti-tumor polypeptides - prepared using recombinant DNA prepared
PT from genomic DNA of human acute leukemia cell THP-1.
XX
XX Disclosure; Fig 4; 63pp; English.
PS
XX The polypeptide is cytotoxic to human tumor cells but not to normal
CC cells. They are also cytotoxic to primary cell cultures obtained
CC from metastasis lesions of patients suffering from striated muscle
CC tumors. They are also resistant to all chemotherapeutic agents.
CC See also AAN70073-75, AAP70077-78 and AAP95592.
XX
XX Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 other;
SQ
Query Match 100.0%; Score 43; DB 8; Length 1200;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 1099 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1141
RESULT 9
AAN90969
ID AAN90969 standard; DNA; 1200 BP.
XX
XX AAN90969;
AC
XX 11-MAR-1990 (first entry)
DT
XX Part of gene for anti-cancer peptide.
DE
XX Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
KM
XX

```
OS   THP-1 cells.
XX
PN   JP01095784-A.
XX
PD   13-APR-1989.
XX
PF   06-OCT-1987;    87JP-0252174.
XX
PR   06-OCT-1987;    87JP-0252174.
XX
PA   (SENG ) SEN G.
XX
DR   WPI; 1989-154899/21.
XX
PT   Novel DNA, plasmid and polypeptide(s)
XX   - useful as anticarcinogenic agents
XX
PS   Fig 2; ; 17pp; Japanese.
XX
CC   Gene for anticarcinogenic peptide. It is genomic DNA or cDNA from THP-1
CC   cells.
XX
SQ   Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 other;

Query Match          100.0%; Score 43; DB 10; Length 1200;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
    |||||||
Db   1099 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1141

RESULT 10
AAN60558
ID   AAN60558 standard; DNA; 1275 BP.
XX
AC   AAN60558;
XX
DT   28-JUL-1991 (first entry)
XX
DE   Sequence encoding mature human tumour necrosis factor (hTNF) mutein
DE   Ser 69 in PAW731.
XX
KM   Antitumour; anticancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key
FT   CDS          Location/Qualifiers
FT              1..474
FT              /*tag= a
XX
PN   WO8604606-A.
XX
PD   14-AUG-1986.
XX
PF   03-FEB-1986;    86WO-US00236.
XX
PR   07-FEB-1985;    85US-0698939.
PR   19-OCT-1982;    82US-0435154.
PR   15-APR-1983;    83US-0486162.
PR   20-DEC-1983;    83US-0564224.
PR   15-OCT-1984;    84US-0661026.
PR   07-FEB-1985;    85US-0695934.
XX
PA   (CETU ) CETUS CORP.
XX
PI   Mark DF, Lin LS, Lu SDY, Wang AM;
XX
DR   WPI; 1986-225458/34.
DR   P-PSDB; AAP60656.
XX
PT   New synthetic muteins of human tumour necrosis factor protein -
```

```
PT   are obtd. by direct mutagenesis and retain antitumour activity
XX
PS   Disclosure; Fig 3a; 47pp; English.
XX
CC   The sequence encoding TNF produced by the promyelocytic leukemia
CC   cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in
CC   E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
CC   the TNF sequence appears to be involved in disulphide linkages. The
CC   patentors claim a novel synthetic mutein of a biologically active
CC   hTNF protein, having at least one cysteine residue free from a
CC   disulphide link and non-essential to the activity and having at
CC   least one of the cysteine residues deleted or replaced by another AA.
CC   Plasmid PAW731 (Ser 69) is claimed.
XX
SQ   Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 other;

Query Match          100.0%; Score 43; DB 7; Length 1275;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
    |||||||
Db   697 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 739

RESULT 11
AAN60363
ID   AAN60363 standard; DNA; 1323 BP.
XX
AC   AAN60363;
XX
DT   19-JUN-1991 (first entry)
XX
DE   Sequence encoding human tumour necrosis factor.
DE   hTNF; tumour; cancer; interferon; ds.
XX
KM   Homo sapiens.
XX
OS   Homo sapiens.
XX
FH   Key
FT   CDS          Location/Qualifiers
FT              1..534
FT              /*tag= a
FT   sig_peptide  1..60
FT              /*tag= b
FT   mat_peptide  61..534
FT              /*tag= c
XX
PN   EP168214-A.
XX
PD   15-JAN-1986.
XX
PF   03-JUL-1985;    85EP-0304758.
XX
PR   03-DEC-1984;    84US-0677454.
PR   05-JUL-1984;    84US-0627959.
PR   05-JUL-1984;    84US-0628059.
PR   05-JUL-1984;    84US-0628060.
PR   03-DEC-1984;    84US-0677156.
PR   03-DEC-1984;    84US-0677257.
PR   25-JUL-1984;    84US-0627969.
PR   03-DEC-1984;    84US-0677267.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;
XX
DR   WPI; 1986-015483/03.
DR   P-PSDB; AAP60417.
XX
PT   Pure tumour necrosis factor and mutant forms - new DNA coding
XX   sequences and transformed cells.
```


PS Claim 20; Fig 10; 90pp; English.
XX
CC Sequence encodes the pure human tumour necrosis factor, mutants of
CC which are covered by the claims. TNF and mutants are useful in
CC treating tumours, especially in tandem with interferon. The
CC encoding sequence may be used to create plasmid pTRXAPTNF, allowing
CC transformation of an E.coli host for the expression of TNF.
XX
SQ Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 other;
Query Match 100.0%; Score 43; DB 7; Length 1323;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCAAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGA 43
|||||
Db 754 TCAAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGA 796
RESULT 12
AAF21085
ID AAF21085 standard; DNA; 1324 BP.
XX
AC AAF21085;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2652.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PE 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 887; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
XX

CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impaired respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;
Query Match 100.0%; Score 43; DB 21; Length 1324;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCAAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGA 43
|||||
Db 755 TCAAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGA 797
RESULT 13
AAA34963
ID AAA34963 standard; DNA; 1324 BP.
XX
AC AAA34963;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2652.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PE 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 814-815; 1343pp; English.
XX

CC E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
CC the TNF sequence appears to be involved in disulphide linkages. The
CC patentors claim a novel synthetic mutein of a biologically active
CC hTNF protein, having at least one cysteine residue free from a
CC disulphide link and non-essential to the activity and having at
CC least one of the cysteine residues deleted or replaced by another AA.
CC Plasmid pAW731 (Ser 69) is claimed.

XX
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 other;

Query Match 100.0%; Score 43; DB 7; Length 1585;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
DB 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

Search completed: July 1, 2003, 20:54:33
Job time : 100.163 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:41:41 ; Search time 765.81 Seconds
(without alignments)
909.372 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaactggggcctccagaa.....actgggcctacagcttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlov:*
5: em_estmu:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	248	14 T29839	T29839 EST97164 Hu
2	43	100.0	722	14 BQ007008	BQ007008 UI-H-E11-
3	43	100.0	1014	9 AL543083	AL543083 AL543083
4	35.2	81.9	581	9 AI242177	AI242177 qh81908.x
5	33.6	78.1	564	9 AA699697	AA699697 z178f12.s
6	28	65.1	561	12 BG232086	BG232086 naf32e06.

C	7	25	58.1	660	9	AL575811	AL575811
C	8	24.8	57.7	431	17	AQ459761	AQ459761 HS_5125_A
	9	24	55.8	594	14	N26123	N26123 yx90h08.s1
	10	23.8	55.3	163	12	BF737938	BF737938 CM2-KT003
	11	23.6	54.9	172	12	BF855413	BF855413 RC4-FN020
	12	23.4	54.4	763	14	BQ445871	BQ445871 UI-H-EU1-
C	13	23.2	54.0	1025	14	BQ229625	BQ229625 AGENCOURT
C	14	23.2	54.0	1057	13	BM550588	BM550588 AGENCOURT
	15	23	53.5	563	9	AA436782	AA436782 zv70g11.r
	16	23	53.5	710	17	AZ960058	AZ960058 2M0227P20
	17	23	53.5	752	9	AJ394287	AJ394287 AJ394287
	18	22.8	53.0	403	14	R66993	R66993 y126a03.s1
	19	22.8	53.0	483	10	AW124522	AW124522 UI-M-BH2.
	20	22.8	53.0	710	12	BE887866	BE887866 601511252
	21	22.6	52.6	906	12	BF276273	BF276273 GA_Eb002
	22	22.6	52.6	1061	12	BG242594	BG242594 602354007
	23	22.4	52.1	454	12	BF906910	BF906910 RC3-ST019
C	24	22.4	52.1	766	14	BO881306	BO881306 AGENCOURT
C	25	22.4	52.1	1023	10	BE540979	BE540979 601064322
C	26	22.2	51.6	262	9	AA076881	AA076881 7B04E10 C
	27	22.2	51.6	407	10	BE245928	BE245928 TCBAPI033
	28	22.2	51.6	437	10	BB839661	BB839661 BB839661
	29	22.2	51.6	803	12	BG105346	BG105346 602312447
	30	22.2	51.2	414	17	AZ891586	AZ891586 RPCI-24-2
	31	22	51.2	466	14	R63875	R63875 y121d12.s1
	32	22	51.2	559	12	BG487265	BG487265 df95b02.y
	33	22	51.2	571	10	BE287225	BE287225 601093933
	34	22	51.2	736	12	BG843692	BG843692 102400360
	35	22	51.2	865	12	BG326842	BG326842 602425726
C	36	21.8	50.7	457	12	BG521116	BG521116 ps55a07.y
C	37	21.8	50.7	474	12	BG521132	BG521132 ps55d03.y
C	38	21.8	50.7	486	12	BG520557	BG520557 ps26h03.y
C	39	21.8	50.7	523	10	AW766053	AW766053 da81f04.y
C	40	21.8	50.7	550	12	BG232776	BG232776 ps01c06.y
C	41	21.8	50.7	556	9	AJ397890	AJ397890 AJ397890
C	42	21.8	50.7	560	10	BE665704	BE665704 154832 MA
C	43	21.8	50.7	585	13	BM190565	BM190565 POSM01000
C	44	21.8	50.7	587	17	CNS01Y49	AL172530 Tetradon
C	45	21.8	50.7	834	13	BI753139	BI753139 603025991

ALIGNMENTS

RESULT 1	T29839	248 bp	mRNA	linear	EST 06-SEP-1995
LOCUS	EST97164	Human Testis	Homo sapiens	CDNA 5'	end similar to tumor
DEFINITION	necrosis factor, alpha (HT:1190), mRNA sequence.				
ACCESSION	T29839				
VERSION	T29839.1	GI:611937			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Adams,M.D., Kerlavage,A.R., Fleschmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.M., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinklejr,P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrle,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Weisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wang,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and				

TITLE Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
MEDLINE 96026280
COMMENT Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gathersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org)
Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers
1..248

BASE COUNT 63 a 65 c 60 g 57 t 3 others
ORIGIN
/organism="Homo sapiens"
/db_xref="ATCC (inhost):107667"
/db_xref="taxon:9606"
/clone_lib="Human Testis"
/note="Organ: testis"

Query Match 100.0%; Score 43; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTACCTGGGCTACAGCTTTGA 43
|||||
Db 62 TCAAACTGGGGCTCCAGAACTCACTACCTGGGCTACAGCTTTGA 104

RESULT 2
BQ007008/c 722 bp mRNA linear EST 26-MAR-2002
LOCUS UI-H-E11-azb-j-22-0-UI.s1 NCI_CGAP_E11 Homo sapiens cDNA clone
IMAGE:5846517 3', mRNA sequence.
ACCESSION BQ007008
VERSION BQ007008.1 GI:19731908
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 722)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Location/Qualifiers
1..722

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5846517"
/clone_lib="NCI_CGAP_E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: p7T13-Pac (Pharmacia)"

with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_E11 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p7T13-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
ACACTGCAC.
TAG_LIB=UI-H-E11
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTGCAC"

BASE COUNT 204 a 162 c 164 g 190 t 2 others
ORIGIN
Query Match 100.0%; Score 43; DB 14; Length 722;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTACCTGGGCTACAGCTTTGA 43
|||||
Db 591 TCAAACTGGGGCTCCAGAACTCACTACCTGGGCTACAGCTTTGA 549

RESULT 3
AL543083/c 1014 bp mRNA linear EST 16-FEB-2001
LOCUS AL543083 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI002YE03 3
DEFINITION prime, mRNA sequence.
ACCESSION AL543083
VERSION AL543083.1 GI:12875561
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 1014)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Location/Qualifiers
1..1014

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI002YE03"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 265 a 232 c 281 g 234 t 2 others
ORIGIN

Query Match 100.0%; Score 43; DB 9; Length 1014;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTACCTGGGCTACAGCTTTGA 43

Db 548 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 506
|||||
RESULT 4
LOCUS AI242177/c 581 bp mRNA linear EST 01-DEC-1998
DEFINITION qh81908.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens CDNA
clone IMAGE:1851134 3' similar to gb:M10988 TUMOR NECROSIS FACTOR
PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI242177
VERSION AI242177.1 GI:3837574
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1280 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 463.
FEATURES
source
1. 581
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1851134"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen 1NFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AACTGGAAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 179 a 130 c 135 g 137 t
ORIGIN

Query Match 81.9%; Score 35.2; DB 9; Length 581;
Best Local Similarity 92.5%; Pred. No. 0.0079;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 AACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 43
|||
Db 574 AAACGTGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 535
|||||

RESULT 5
LOCUS AA699697/c 564 bp mRNA linear EST 19-DEC-1997
DEFINITION z178f12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens CDNA
clone IMAGE:446927 3' similar to gb:M10988 TUMOR NECROSIS FACTOR
PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AA699697
VERSION AA699697.1 GI:2703844
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 564)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Thelking, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 397.
FEATURES
source
1. 564
/organism="Homo sapiens"
/db_xref="GDB:1351184"
/db_xref="taxon:9606"
/clone="IMAGE:446927"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen 1NFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AACTGGAAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 176 a 123 c 138 g 127 t
ORIGIN

Query Match 78.1%; Score 33.6; DB 9; Length 564;
Best Local Similarity 90.0%; Pred. No. 0.031;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTT 40
|||||
Db 561 TCAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTT 522
|||||

RESULT 6
LOCUS BG232086/c 561 bp mRNA linear EST 09-FEB-2001
DEFINITION naf32e06.x1 Soares_NPBMC Homo sapiens CDNA clone IMAGE:4142698 3',
mRNA sequence.
ACCESSION BG232086
VERSION BG232086.1 GI:12727241
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 561)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima
Bonaldo, Ph.D.

RESULT 9
N26123
LOCUS
DEFINITION
Yx90h08.s1 Soares melanocyte 2NbHM Homo sapiens CDNA clone
IMAGE:269055 3' similar to gb|M87890|HUMALCE124 Human carcinoma
cell-derived Alu RNA transcript, (cRNA); gb:X14008_rnal LYSOZYME C
PRECURSOR (HUMAN); contains Alu repetitive element;; mRNA sequence.
N26123
VERSION
N26123.1 GI:1140471
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 594)
AUTHORS
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maira,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 427
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 427.
location/Qualifiers
1. 594
/organism="Homo sapiens"
/db_xref="GDB:3878697"
/db_xref="taxon:9606"
/clone_1ib="IMAGE:269055"
/clone_1ib="Soares melanocyte 2NbHM"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA
was primed with a Not I - oligo(dt) primer [5',
TGTTACCAATCTGAGAGTGGAGCGCGCAGTTTCTTTTCTTTT 3'],
double-stranded CDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT
158 a 135 c 110 g 186 t 5 others
ORIGIN
Query Match 55.8%; Score 24; DB 14; Length 594;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 4 AACTGGGGCTCCAGACTACACTGGGGCTACAGCTTGA 43
1 11 11111111 1111 11111 11111 1 111
Db 411 ACCTCAGGCTCCAAACTGGCTGGGATTACAGGTGTGA 450
RESULT 10
BF737938 163 bp mRNA linear EST 10-JAN-2001
LOCUS
DEFINITION
CM2-KT0031-141200-628-c08 KT0031 Homo sapiens CDNA, mRNA sequence.
BF737938
ACCESSION
BF737938.1 GI:12064614
VERSION
EST..
KEYWORDS
human.
SOURCE

ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 163)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&tl2=CM2-KT0031-
141200-628-c08&tl3=2000-12-14&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 4
High quality sequence stop: 77.
location/Qualifiers
1. 163
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="KT0031"
/dev_stage="Adult"
/note="Organ: bladder_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
BASE COUNT
34 a 50 c 35 g 44 t
ORIGIN
Query Match 55.3%; Score 23.8; DB 12; Length 163;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 5 ACTGGGGCTCCAGACTACACTGGGGCTACAGCT 39
1 1111 111 11 1 11111111 11 11111
Db 1 ACTGGTGCATCATAGCTACTGGGGCTCCAGCT 35
RESULT 11
BF855413 172 bp mRNA linear EST 16-JAN-2001
LOCUS
DEFINITION
RC4-FN0203-121100-011-b01 FN0203 Homo sapiens CDNA, mRNA sequence.
BF855413
ACCESSION
BF855413.1 GI:12243157
VERSION
EST.
KEYWORDS
human.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 172)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL MEDLINE COMMENT

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4<2=RC4-FN0203-
121100-011-b01&t3=2000-11-12&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 65
High quality sequence stop: 172.

FEATURES source location/Qualifiers

1..172

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="FN0203"
/dev_string="Adult"

/note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI ; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 47 a 46 c 38 g 41 t

ORIGIN

Query Match 54.9%; Score 23.6; DB 12; Length 172;
.Best Local Similarity 76.3%; Pred. No. 1.1e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

CY 2 CAAACTGGGCGCTCCAGACTCACTGGGCCCTACAGCT 39
||| ||| ||| ||| ||| ||| ||| ||| ||| | |||

Db 133 CACAGTGTGTCCACCACGAGCTCAGCTGTGGCCTTGAACT 170

RESULT 12

LOCUS BQ445871 763 bp mRNA linear EST 29-MAY-2002

DEFINITION UI-H-EUI-azy-m-09-0-UI.s1 NCI_CGAP Clt1 Homo sapiens CDNA clone.

VERSION BQ445871

KEYWORDS BQ445871.1 GI:21248983

SOURCE EST.

ORGANISM human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 763)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA sequence: 1-103, >(GAAA)n#simple_repeat (matched complement) 104-402, >ALU (matched complement) 318-427, >ALU (matched complement) 605-761, >MLT2B2

Seq primer: M13 FORWARD

FEATURES	POLYA-NO.
SOURCE	Location/Qualifiers 1. .763 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="UI-H-EU1-azy-m-09-0-UI" /clone_1lb="NCI_CGAP_Ct1" /tissue_type="Osteoarthritic Cartilage" /dev_stage="Adult" /lab_host="DH10B (Life Technologies)" /note="Organ: Knee; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_Ct1 is a normalized cDNA library containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCAGCGT. TAG_LIB=UI-H-EU1 TAG_TISSUE=osteoarthritic cartilage TAG_SEQ=TGATCAGCGT"
BASE COUNT	160 a 171 c 157 g 274 t 1 others
ORIGIN	
Query Match	54.4%; Score 23.4; DB 14; Length 763;
Best Local Similarity	73.2%; Pred. No. 1.9e+02;
Matches	30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY	3 AAACGGGGCCCTCCAGAACTCACTGGGCCCTACAGCTTTGA 43
Db	1 11111 11 1111111 1111 1111 1111 147 ACACTGGTGCATCATGACTCACTGAAGCCTGCAGCCTTGA 187
RESULT 13	
BQ229625/c	LOCUS BQ229625 1025 bp mRNA linear EST 02-MAY-2002
DEFINITION	AGENCOURT_7558467 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6046767
ACCESSION	BQ229625
VERSION	BQ229625.1 GI:20411025
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1025)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs@email.nih.gov Tissue Procurement: ATCC/DCTD/DTF CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM13293 row: b column: 16 High quality sequence stop: 419.
FEATURES	Location/Qualifiers 1. .1025 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6046767" /clone_1lb="NIH_MGC_72" /tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 196 a 363 c 256 g 209 t 1 others
ORIGIN

Query Match 54.0%; Score 23.2; DB 14; Length 1025;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 8 GGGGCTCCAGACTCACTGGGCTACAGCTTTGA 43
||||| | ||||| ||||| ||||| | |||||
Db 744 GGGGCGCGAGACTCACTGGGCGGAGTCTGTGA 709

RESULT 14
BM550588/c 1057 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6585260 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471663
DEFINITION 5', mRNA sequence.
ACCESSION BM550588
VERSION BM550588.1 GI:18786913
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1057)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1980 row: g column: 24
High quality sequence stop: 770.

FEATURES
source location/Qualifiers
1..1057

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5471663"
/clone_1lb="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."

BASE COUNT 295 a 285 c 272 g 202 t 3 others
ORIGIN

Query Match 54.0%; Score 23.2; DB 13; Length 1057;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 8 GGGGCTCCAGACTCACTGGGCTACAGCTTTGA 43
||||| | ||||| ||||| ||||| | |||||
Db 1033 GGGGCTTCAGAGCTCACTGGGCGATGCTGTTTCA 998

RESULT 15

AA436782 563 bp mRNA linear EST 30-MAY-1997
LOCUS zv70g11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
DEFINITION IMAGE:759044 5' similar to contains Alu repetitive element; contains
element MER22 repetitive element ;, mRNA sequence.

ACCESSION AA436782
VERSION AA436782.1 GI:2141696
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 563)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Maira, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,
, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE Contact: Wilson RK
JOURNAL Washington University School of Medicine
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 492.

FEATURES
source location/Qualifiers
1..563

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:759044"
/clone_1lb="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAGTGGAGCGCGCTTAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 158 a 150 c 159 g 96 t
ORIGIN

Query Match 53.5%; Score 23; DB 9; Length 563;
Best Local Similarity 74.4%; Pred. No. 2.5e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCTCCAGACTCACTGGGCTACAGCT 39
|| | ||||| ||||| | ||||| ||||| |||||
Db 449 TCCAATTTGGGATCCAGAGCCACCTGGGCTGCAGGT 487

Search completed: July 1, 2003, 22:11:28
Job time : 772.81 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:43:24 ; Search time 20.7687 Seconds
(without alignments)
634.950 Million cell updates/sec

Title: US-09-801-371A-2

Perfect score: 43

Sequence: 1 tcaactgggcctccagaa.....actgggcctacagcttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	1643	4	US-08-880-342-36 Sequence 36, Appl
2	43	100.0	1643	4	US-09-505-250-4 Sequence 4, Appl
3	43	100.0	3634	3	US-09-166-186-1 Sequence 1, Appl
4	43	100.0	3634	4	US-09-313-932-1 Sequence 1, Appl
5	43	100.0	3634	4	US-09-109-663-34 Sequence 34, Appl
6	21	48.8	771	5	PCT-US95-12987-1 Sequence 1, Appl
7	21	48.8	771	5	PCT-US95-12987-3 Sequence 5, Appl
8	21	48.8	771	5	PCT-US95-12987-5 Sequence 1, Appl
9	20.8	48.4	861	1	US-08-409-731A-1 Sequence 1, Appl
10	20.8	48.4	861	2	US-08-470-298B-1 Sequence 1, Appl
11	20.8	48.4	861	2	US-09-023-073A-1 Sequence 1, Appl
12	20.8	48.4	861	4	US-09-361-737-1 Sequence 1, Appl
13	20.8	48.4	944	2	US-08-820-825-1 Sequence 1, Appl
14	20.8	48.4	944	4	US-09-307-817-1 Sequence 1, Appl
15	20.8	48.4	944	4	US-09-734-036-1 Sequence 1, Appl
16	20.8	48.4	957	3	US-08-899-031-2 Sequence 2, Appl
17	20.8	48.4	65042	4	US-09-784-316-3 Sequence 3, Appl
18	20	46.5	20	3	US-09-166-186-32 Sequence 32, Appl
19	20	46.5	20	3	US-09-166-186-212 Sequence 212, App
20	20	46.5	20	3	US-09-166-186-213 Sequence 213, App
21	20	46.5	20	3	US-09-166-186-214 Sequence 214, App
22	20	46.5	20	4	US-09-313-932-32 Sequence 32, Appl
23	20	46.5	20	4	US-09-313-932-212 Sequence 212, App
24	20	46.5	20	4	US-09-313-932-213 Sequence 213, App
25	20	46.5	20	4	US-09-313-932-214 Sequence 214, App
26	20	46.5	20	4	US-09-313-932-354 Sequence 354, App
27	20	46.5	20	4	US-09-313-932-357 Sequence 357, App

c	28	20	46.5	20	4	US-09-313-932-358	Sequence 358, App
c	29	20	46.5	20	4	US-09-313-932-361	Sequence 361, App
c	30	20	46.5	20	4	US-09-313-932-468	Sequence 468, App
c	31	19.8	46.0	3431	4	US-09-632-098-1	Sequence 1, Appl
c	32	19.8	46.0	3468	4	US-09-632-098-3	Sequence 3, Appl
c	33	19.8	46.0	4695	2	US-08-231-193A-57	Sequence 57, Appl
c	34	19.8	46.0	4695	2	US-08-231-193A-57	Sequence 57, Appl
c	35	19.8	46.0	4695	3	US-08-940-086A-57	Sequence 57, Appl
c	36	19.8	46.0	4695	4	US-08-940-086A-57	Sequence 57, Appl
c	37	19.8	46.0	4695	4	US-08-935-105A-57	Sequence 57, Appl
c	38	19.8	46.0	4695	4	US-09-648-797-57	Sequence 57, Appl
c	39	19.4	45.1	2061	4	US-09-653-839-7	Sequence 7, Appl
c	40	19.4	45.1	2109	4	US-09-653-839-5	Sequence 5, Appl
c	41	19.4	45.1	2156	1	US-08-178-477B-31	Sequence 31, Appl
c	42	19.4	45.1	2156	4	US-09-304-121-1	Sequence 1, Appl
c	43	19.4	45.1	2172	4	US-09-653-839-3	Sequence 3, Appl
c	44	19.4	45.1	2220	4	US-09-653-839-1	Sequence 1, Appl
c	45	19.4	45.1	2458	4	US-09-513-783A-175	Sequence 175, App

ALIGNMENTS

RESULT 1
US-08-880-342-36
Sequence 36, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: TNF CDNA HSTNFR (EMBL Accession
; INDIVIDUAL ISOLATE: #X01394)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 153..851
; US-08-880-342-36

Query Match      100.0%; Score 43; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGACTCAGCTGGGCTACAGCTTTGA 43
Db      1074 TCAAACTGGGGCCTCCAGACTCAGCTGGGCTACAGCTTTGA 1116

RESULT 2
US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (153)..(854)
; US-09-505-250-4

Query Match      100.0%; Score 43; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGACTCAGCTGGGCTACAGCTTTGA 43
Db      1074 TCAAACTGGGGCCTCCAGACTCAGCTGGGCTACAGCTTTGA 1116

RESULT 3
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- $\alpha$  EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
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; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
; TITLE: homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
; US-09-166-186-1

Query Match      100.0%; Score 43; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGACTCAGCTGGGCTACAGCTTTGA 43
Db      2812 TCAAACTGGGGCCTCCAGACTCAGCTGGGCTACAGCTTTGA 2854

RESULT 4
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- $\alpha$  EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
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FEATURE:
NAME/KEY: Intron
LOCATION: (982)..(1588)
FEATURE:
NAME/KEY: exon
LOCATION: (1589)..(1634)
FEATURE:
NAME/KEY: Intron
LOCATION: (1635)..(1821)
FEATURE:
NAME/KEY: exon
LOCATION: (1822)..(1869)
FEATURE:
NAME/KEY: Intron
LOCATION: (1870)..(2070)
FEATURE:
NAME/KEY: exon
LOCATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Naylor, S.L.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Jarrett-Nedwin, J.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor genes:
TITLE: structure, homology and chromosomal localization
JOURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1

Query Match 100.0%; Score 43; DB 4; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAACTGGGGCCTCCAGACTCACTGGGGCTTGA 43
|||||
DB 2812 TCAACTGGGGCCTCCAGACTCACTGGGGCTTGA 2854

RESULT 5
US-09-109-663-34
Sequence 34, Application US/09109663
Patent No. 6277981
GENERAL INFORMATION:
APPLICANT: Tu, Guang-Chou
APPLICANT: Israel, Yedy
TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
FILE REFERENCE: 9855-301
CURRENT APPLICATION NUMBER: US/09/109,663
CURRENT FILING DATE: 1998-07-03
EARLIER APPLICATION NUMBER: 60/051,705
EARLIER FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 3634
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: TNF(alpha) CDNA
US-09-109-663-34

Query Match 100.0%; Score 43; DB 4; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAACTGGGGCCTCCAGACTCACTGGGGCTTGA 43
|||||
DB 2812 TCAACTGGGGCCTCCAGACTCACTGGGGCTTGA 2854

RESULT 6
PCT-US95-12987-1
Sequence 1, Application PC/TUS9512987
GENERAL INFORMATION:
APPLICANT: LAFEMINA, R.
APPLICANT: SARDANA, V.
APPLICANT: VELOSKI, C.
TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROY D. MEREDITH
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12987
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEREDITH, ROY D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 19262 PCT
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-12987-1

Query Match 48.8%; Score 21; DB 5; Length 771;
Best Local Similarity 73.0%; Pred. No. 9;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TCAACTGGGGCCTCCAGACTCACTGGGGCTTGA 37
|||||
DB 539 TCACACACGGGTTTCAGACTCAGCGCGCGGACCG 575

RESULT 7
PCT-US95-12987-3
Sequence 3, Application PC/TUS9512987
GENERAL INFORMATION:
APPLICANT: LAFEMINA, R.
APPLICANT: SARDANA, V.
APPLICANT: VELOSKI, C.
TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROY D. MEREDITH
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA


```
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 94..414
; US-08-470-298B-1

Query Match      48.4%; Score 20.8; DB 2; Length 861;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      11 GCCTCAGACTGCTGGGGCTACAGCTTTG 42
          ||||| | ||||| ||| |||||
Db      96 GCCTCCACCTGCTGCTACTACCGCTTTG 127

RESULT 11
US-09-023-073A-1
; Sequence 1, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,737
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/023,073
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Wale, Michele M.
; REGISTRATION NUMBER: P-43,975
; REFERENCE/DOCKET NUMBER: PF175D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 94..414
; US-09-023-073A-1
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,073A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Wale, Michele M.
; REGISTRATION NUMBER: P-43,975
; REFERENCE/DOCKET NUMBER: PF175D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 94..414
; US-09-023-073A-1

Query Match      48.4%; Score 20.8; DB 2; Length 861;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      11 GCCTCAGACTGCTGGGGCTACAGCTTTG 42
          ||||| | ||||| ||| |||||
Db      96 GCCTCCACCTGCTGCTACTACCGCTTTG 127
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RESULT 12
US-09-361-737-1
; Sequence 1, Application US/09361737
; Patent No. 6287812
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,737
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/023,073
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Wale, Michele M.
; REGISTRATION NUMBER: P-43,975
; REFERENCE/DOCKET NUMBER: PF175D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 94..414
US-09-361-737-1

Query Match 48.4%; Score 20.8; DB 4; Length 861;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 11 GCCTCCAGACTGCTGCGGCTACAGCTTTG 42
||||| | ||||| ||||| |||||
Db 96 GCCTCCCACTGCTGCTACTACCGCTTTG 127

RESULT 13

US-08-820-825-1
Sequence 1, Application US/08820825
Patent No. 5945309

GENERAL INFORMATION:

APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/820,825

FILING DATE: 19-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF2222

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 944 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 94..498

US-08-820-825-1

Query Match 48.4%; Score 20.8; DB 2; Length 944;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 11 GCCTCCAGACTGCTGCGGCTACAGCTTTG 42
||||| | ||||| ||||| |||||
Db 96 GCCTCCCACTGCTGCTACTACCGCTTTG 127

RESULT 14

US-09-307-817-1
Sequence 1, Application US/09307817
Patent No. 6232291

GENERAL INFORMATION:

APPLICANT: NI, JIAN

APPLICANT: YU, GUO-LIANG

APPLICANT: GENTZ, REINER L.

APPLICANT: DILON, PATRICK

TITLE OF INVENTION: CYTOSTATIN III

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/307,817

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/820,825

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF2222

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 944 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 94..498

US-09-307-817-1

Query Match 48.4%; Score 20.8; DB 4; Length 944;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 11 GCCTCCAGACTGCTGCGGCTACAGCTTTG 42
||||| | ||||| ||||| |||||
Db 96 GCCTCCCACTGCTGCTACTACCGCTTTG 127

RESULT 15

US-09-734-036-1
Sequence 1, Application US/09734036
Patent No. 6413726

GENERAL INFORMATION:

APPLICANT: NI, JIAN

APPLICANT: YU, GUO-LIANG

APPLICANT: GENTZ, REINER L.

APPLICANT: DILON, PATRICK

TITLE OF INVENTION: CYTOSTATIN III

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,036
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/307,817
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 944 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 94..498
US-09-734-036-1

Query Match 48.4%; Score 20.8; DB 4; Length 944;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 11 GCCTCCAGACTCCTGCGGCTACAGCTTTG 42
||||| | ||||| | |||||
Db 96 GCCTCCCAACTCCTGCGCTACTACCGCTTTG 127

Search completed: July 1, 2003, 22:12:42
Job time : 21.7687 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:48:50 ; Search time 56.7483 Seconds
(without alignments)
1124.814 Million cell updates/sec

Title: US-09-801-371A-2

Perfect score: 43
Sequence: 1 tcaactggggcctccagaa.....actggggcctacagcttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1055720 seqs, 742224136 residues

Total number of hits satisfying chosen parameters: 2111440

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	43	100.0	43	9	US-09-801-371A-2	Sequence 2, Appli
2	43	100.0	43	9	US-09-801-371A-6	Sequence 6, Appli
3	43	100.0	50	9	US-09-801-371A-8	Sequence 8, Appli
4	43	100.0	81	9	US-09-801-371A-7	Sequence 7, Appli
5	43	100.0	104	9	US-09-801-371A-1	Sequence 1, Appli
6	43	100.0	104	9	US-09-801-371A-5	Sequence 5, Appli
7	43	100.0	1643	9	US-10-218-547-3	Sequence 3, Appli
8	43	100.0	1643	9	US-10-272-411-4	Sequence 4, Appli
9	43	100.0	1643	9	US-10-272-328A-4	Sequence 1, Appli
10	43	100.0	3634	9	US-09-824-322B-1	Sequence 34, Appli
11	43	100.0	3634	9	US-09-932-300-34	Sequence 6223, Ap
12	35	81.4	418	9	US-09-796-692-6223	Sequence 6223, Ap
13	35	81.4	418	9	US-10-040-862-6223	Sequence 6223, Ap
14	30.6	71.2	51	9	US-09-801-371A-10	Sequence 1127, Ap
15	23	53.5	260	9	US-09-535-459-1127	Sequence 11, Appl
16	22.2	51.6	27	9	US-09-801-371A-11	Sequence 10563, A
17	22	51.2	363	10	US-09-783-590-10563	Sequence 146, App
18	21.4	49.8	406	10	US-09-560-863-146	Sequence 72, Appl
19	21.4	49.8	1274	9	US-09-981-876-72	

C	20	21.4	49.8	1274	9	US-09-148-545-72	Sequence 72, Appl
C	21	21.4	49.8	1296	9	US-09-981-876-126	Sequence 126, App
C	22	21.4	49.8	1296	9	US-09-148-545-126	Sequence 126, App
C	23	21.4	49.8	1343	10	US-09-925-300-779	Sequence 779, App
C	24	21.4	49.8	3113	9	US-09-764-891-5580	Sequence 5580, Ap
	25	21.4	49.8	24707	9	US-10-274-968-3	Sequence 3, Appli
	26	21.4	49.8	24707	10	US-09-740-027-3	Sequence 3, Appli
	27	21	48.8	768	9	US-10-214-932-97	Sequence 97, Appl
	28	20.8	48.4	426	9	US-09-918-995-5224	Sequence 5224, Ap
	29	20.8	48.4	461	9	US-09-918-995-15882	Sequence 15882, A
C	30	20.8	48.4	493	10	US-09-783-590-4012	Sequence 4012, Ap
C	31	20.8	48.4	551	10	US-09-737-149-13	Sequence 13, Appl
	32	20.8	48.4	557	10	US-09-833-381-551	Sequence 551, App
	33	20.8	48.4	817	10	US-09-737-149-15	Sequence 15, Appl
	34	20.8	48.4	861	10	US-09-901-436A-1	Sequence 1, Appli
	35	20.8	48.4	944	12	US-10-153-740-1	Sequence 1, Appli
	36	20.8	48.4	957	9	US-10-032-366-2	Sequence 2, Appli
	37	20.8	48.4	1241	9	US-10-098-841-118	Sequence 118, App
C	38	20.8	48.4	1327	10	US-09-833-381-1346	Sequence 1346, Ap
	39	20.8	48.4	65042	9	US-10-229-124-3	Sequence 3, Appli
C	40	20.8	48.4	143306	10	US-09-729-920-3	Sequence 3, Appli
	41	20.4	47.4	239	10	US-09-998-598-1944	Sequence 1944, Ap
	42	20.4	47.4	374	9	US-10-046-935-438	Sequence 438, App
	43	20.4	47.4	374	9	US-09-878-178-438	Sequence 438, App
	44	20.4	47.4	374	9	US-10-146-502-438	Sequence 438, App
C	45	20.4	47.4	493	10	US-09-864-761-5346	Sequence 5346, Ap

ALIGNMENTS

RESULT 1
US-09-801-371A-2
; Sequence 2, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-2

Query Match 100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTTCAGACTCACTGGGGCTTACGCTTTGA 43
Db 1 TCAAACTGGGGCTTCAGACTCACTGGGGCTTACGCTTTGA 43

RESULT 2
US-09-801-371A-6/c
; Sequence 6, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak


```

; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-6

Query Match          100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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DB      43 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1

RESULT 3
US-09-801-371A-8
; Sequence 8, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-8

Query Match          100.0%; Score 43; DB 9; Length 50;
Best Local Similarity 79.1%; Pred. No. 2.4e-08;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      5 UCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 47

RESULT 4
US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
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; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 81
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-7

Query Match          100.0%; Score 43; DB 9; Length 81;
Best Local Similarity 79.1%; Pred. No. 2.4e-08;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

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        :|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      9 UCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 51

RESULT 5
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

Query Match          100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
        |||||||
DB      5 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 47

RESULT 6
US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5
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Query Match 100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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100 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 58

RESULT 7
US-10-218-547-3

; Sequence 3, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-218-547-3

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Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
US-10-272-411-4

; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1

; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

Query Match 100.0%; Score 43; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 9
US-10-272-328A-4

; Sequence 4, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-328A-4

Query Match 100.0%; Score 43; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 10
US-09-824-322B-1

; Sequence 1, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-
; FILE REFERENCE: ISPH-0501
; CURRENT APPLICATION NUMBER: US/09/824,322B
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 09/313,932
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: US 09/166,186
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

NAME/KEY: CDS
LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
NAME/KEY: exon
LOCATION: (615)..(981)
NAME/KEY: Intron
LOCATION: (982)..(1588)
NAME/KEY: exon
LOCATION: (1589)..(1634)
NAME/KEY: Intron
LOCATION: (1635)..(1821)
NAME/KEY: exon
LOCATION: (1822)..(1869)
NAME/KEY: Intron
LOCATION: (1870)..(2070)
NAME/KEY: exon
LOCATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Naylor, S.L.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Jarrett-Nedwin, J.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology and
TITLE: Chromosomal localization
JOURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE ENTRY DATE: 1997-02-17
US-09-824-322B-1

Query Match 100.0%; Score 43; DB 9; Length 3634;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAACTGGGGCTCCAGACTCAGCTGGGCTACAGCTTTGA 43
|||||
Db 2812 TCAACTGGGGCTCCAGACTCAGCTGAGCTTGA 2854

RESULT 11
US-09-932-300-34
Sequence 34, Application US/09932300
Publication No. US20030032788A1
GENERAL INFORMATION:
APPLICANT: GARVER, Eric
APPLICANT: TU, Guang-Chou
APPLICANT: ISRAEL, Yedy
TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION
FILE REFERENCE: 9855-302
CURRENT APPLICATION NUMBER: US/09/932,300
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: US 60/051,705
PRIOR FILING DATE: 1997-07-03
PRIOR APPLICATION NUMBER: US 09/109,663
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 3634
TYPE: DNA
ORGANISM: Homo sapiens
US-09-932-300-34

Query Match 100.0%; Score 43; DB 9; Length 3634;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAACTGGGGCTCCAGACTCAGCTGGGCTACAGCTTTGA 43
|||||
Db 2812 TCAACTGGGGCTCCAGACTCAGCTGAGCTTGA 2854

RESULT 12
US-09-796-692-6223
Sequence 6223, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6223
LENGTH: 418
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (1)
OTHER INFORMATION: n=A,T,C or G
US-09-796-692-6223

Query Match 81.4%; Score 35; DB 9; Length 418;
Best Local Similarity 88.4%; Pred. No. 4.4e-05;
Matches 38; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCAACTGGGGCTCCAGACTCAGCTGGGCTACAGCTTTGA 43
|||||
Db 330 TCAACTGGGGCTCCAGACTCAGCTGAGCTTGA 372

RESULT 13
US-10-040-862-6223
Sequence 6223, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retler, Marc
APPLICANT: Corixa Corporation

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